

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 01:42:24 ; Search time 799.247 Seconds
(without alignments)
5206.064 Million cell updates/sec

Title: US-09-963-827B-3
Perfect score: 96
Sequence: 1 gggagagaggaagggaug.....cgaugacuggaucaccccc 96

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 2199298

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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10: gb_ro.*

11: gb_scs.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_scs.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

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38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	23.8	24.8	138	9	HSA306918	AJ306918 Homo sapi
2	23.2	24.2	78	1	HALTRMI	X03107 Halobacteri
3	23.2	24.2	78	1	HCNET	X03199 Halobacteri
C 4	23.2	24.2	91	9	AY006113	AY006113 Homo sapi
C 5	22.8	23.8	99	1	AB059449	AB059449 Unculture
C 6	22	22.9	181	11	AB059200	AB059200 Sus scrof
C 7	22	22.9	187	11	AU046875	AU046875 Rattus no
8	21.8	22.7	108	6	AR141692	AR141692 Sequence
9	21.8	22.7	108	6	AX638750	AX638750 Sequence
10	21.8	22.7	109	6	AR141696	AR141696 Sequence
11	21.8	22.7	109	6	AX638754	AX638754 Sequence
12	21.8	22.7	133	6	AR141694	AR141694 Sequence
13	21.8	22.7	133	6	AR141698	AR141698 Sequence
14	21.8	22.7	133	6	AX638752	AX638752 Sequence
15	21.8	22.7	133	6	AX638756	AX638756 Sequence
16	21.8	22.7	146	6	AR141693	AR141693 Sequence
17	21.8	22.7	146	6	AR141697	AR141697 Sequence
18	21.8	22.7	146	6	AX638751	AX638751 Sequence
19	21.8	22.7	146	6	AX638755	AX638755 Sequence
20	21.8	22.7	171	6	AR141695	AR141695 Sequence
21	21.8	22.7	171	6	AR141699	AR141699 Sequence
22	21.8	22.7	171	6	AX638753	AX638753 Sequence
23	21.8	22.7	171	6	AX638757	AX638757 Sequence
24	21.6	22.5	78	1	HMTNMMET	X01222 Halococcus
25	21.6	22.5	78	1	SATRNMET	X01223 Sulfolobus
C 26	21.6	22.5	89	9	AY006273	AY006273 Homo sapi
27	21.6	22.5	191	9	HS78B11F	Z66142 H.sapiens C
28	21.4	22.3	107	6	AR184444	AR184444 Sequence
29	21.2	22.1	149	8	AF328872	AF328872 Euterpe e
30	21	21.9	124	9	HS1C7R	Z60309 H.sapiens C
31	20.8	21.7	100	11	G43550	G43550 WIATF-2413-S
32	20.8	21.7	138	10	MMA4LDH5	X02524 M.musculus
33	20.6	21.5	88	6	AR141690	AR141690 Sequence
34	20.6	21.5	88	6	AX638748	AX638748 Sequence
35	20.6	21.5	91	6	A11877	A11877 Nucleotide
C 36	20.6	21.5	91	6	A11878	A11878 Nucleotide
37	20.6	21.5	129	6	AR141702	AR141702 Sequence
38	20.6	21.5	129	6	AX638759	AX638759 Sequence
39	20.6	21.5	141	9	HUMTGMIM	M10957 Human init
40	20.6	21.5	167	6	AR141703	AR141703 Sequence
41	20.6	21.5	167	6	AX638760	AX638760 Sequence
C 42	20.6	21.5	187	6	AX333319	AX333319 Sequence
43	20.4	21.2	77	1	TATRNMET	X01221 Thermoplasm
44	20.4	21.2	156	6	AX181678	AX181678 Sequence
45	20.4	21.2	180	6	I76096	I76096 Sequence 4

ALIGNMENTS

RESULT 1
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LOCUS HSA306918 138 bp DNA linear PRI 04-JAN-2002
DEFINITION Homo sapiens partial SRCRB-S4D gene, exon 7.
ACCESSION AJ306918
VERSION AJ306918.1 GI:18073567
KEYWORDS SRCRB-S4D gene; SRCRB-S4D protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Padilla,O., Pujana,M., Lopez,A., Arman,M., Vila,J., Gimferrer,I.,
Places,L., Vives,J., Estivill,X. and Lozano,F.
TITLE Cloning of a new member of the SRCR-SF


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ORIGIN
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Matches 21; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 50 AUTCAGGACGCUCAUACCGAGGUGGUAUAC 85
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Db 23 ATTCGCGGGCTATACCGGAGATCGTAGTTC 58

RESULT 4
AY006113/c
LOCUS AY006113 91 bp mRNA linear PRI 26-SEP-2000
DEFINITION Homo sapiens clone pbvb203 T cell receptor beta chain mRNA, partial cds.
ACCESSION AY006113 GI:10304544
VERSION AY006113.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 91)
AUTHORS Slachta,C.A., Jeevanandam,V., Goldman,B., Lin,W.L. and Platoucas,C.D.
TITLE Coronary arteries from human cardiac allografts with chronic rejection contain oligoclonal T cells: persistence of identical clonally expanded TCR transcripts from the early post-transplantation period (endomyocardial biopsies) to chronic rejection (coronary arteries)
JOURNAL J. Immunol. 165 (6), 3469-3483 (2000)
MEDLINE 20432336
PUBMED 10975868
REFERENCE 2 (bases 1 to 91)
AUTHORS Slachta,C.A., Jeevanandam,V., Goldman,B.I., Lin,W.L. and Platoucas,C.D.
DIRECT SUBMISSION
TITLE Submitted (31-JUL-2000) Department of Microbiology and Immunology, Temple University School of Medicine, 3400 N. Broad Street, Philadelphia, PA 19140, USA
JOURNAL Philadelphia, PA 19140, USA
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="pbvb203"
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/note="contains Vb2.1 Db2.1 Jb2.3"
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/codon_start=1
/product="T cell receptor beta chain"
/protein_id="AAG15616.1"
/db_xref="GI:10304545"
/translation="DSSFYICSAFSEFREDTDTQYFGTGLTV"

CDS
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Best Local Similarity 45.6%; Pred. No. 4.4e+03;
Matches 31; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 20 GGGACUAUACCGGUAUACGUGCCUCCCAUUCGGAACGCUCAUACCGAGAGUCCA 79
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Db 70 GCGCAAAATACCTGCGTATCTGTCTCCCGTCGGAAGACTAGCACTGCAGATGAGA 11
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QY 80 UAGUACUG 87
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Db 10 AGCTGCTG 3

RESULT 5
AB059449/c
LOCUS AB059449 99 bp DNA linear BCT 25-APR-2001
DEFINITION Uncultured bacterium gene for 16S rRNA, partial sequence, clone:B2_538-14 (B14).
ACCESSION AB059449 GI:13785490
VERSION AB059449.2
KEYWORDS uncultured bacterium
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (sites)
AUTHORS Ueno,Y., Haruta,S., Ishii,M. and Igarashi,Y.
TITLE Changes in Product Formation and Bacterial Community on Carbohydrate Fermentation by Anaerobic Microflora -Effects of Dilution Rate in Continuous Flow Stirred Tank Reactor-
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 99)
AUTHORS Ueno,Y.
TITLE Direct Submission
JOURNAL Submitted (06-APR-2001) Yoshiyuki Ueno, Kajima Technical Research Institute, Bio-environment group; Tbitakyu, 2-19-1, Chofu-shi, Tokyo 182-0036, Japan (E-mail:yoshi-u@katari.kajima.co.jp, Tel:81-424-89-7066(ex.2945), Fax:81-424-89-2896)
COMMENT On Apr 24, 2001 this sequence version replaced gi:13620946.
FEATURES
Location/Qualifiers
1..99
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/db_xref="taxon:77133"
/clone="B2_538-14 (B14)"
/note="DGGF fragment of anaerobic microflora"
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/product="16S ribosomal RNA"

rRNA
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Best Local Similarity 50.0%; Pred. No. 6e+03;
Matches 25; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 28 UACCGCGUAUACGUGCCUCCCAUUCGGAACGCUCAUACCGAGAGUCC 77
||||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 69 TACCGTCTCTTCTTCTGTCGCCCAATCAGAGAAGTTTACACCCGAGGTC 20

RESULT 6
AB059200/c
LOCUS AB059200 181 bp DNA linear STS 19-MAR-2002
DEFINITION Sus scrofa domestica genomic DNA, chromosome 7, 346D10R, sequence tagged site.
ACCESSION AB059200 GI:19570733
VERSION AB059200.1
KEYWORDS STS.
SOURCE Sus scrofa domestica (domestic pig)
ORGANISM Sus scrofa domestica
REFERENCE 1
AUTHORS Kiuchi,S., Inage,Y., Hiraiwa,H., Uenishi,H. and Yasue,H.
TITLE Assignment of 280 swine genomic inserts including 31 microsatellites from BAC clones to the swine RH map (IMPRH map)
JOURNAL Mamm. Genome 13 (2), 80-88 (2002)
MEDLINE 21886643
PUBMED 11889555
REFERENCE 2 (bases 1 to 181)
AUTHORS Kiuchi,S.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2001) Sachiko Kiuchi, National Institute of Agrobiological Sciences, Genome Research Group; 2 Ikenodai, Kunitzaki-machi, Inaashiki-gun, Ibaraki 305-0901, Japan.
```

(E-mail: sachikok@aaffrc.go.jp, Tel: 81-298-38-8664,
Fax: 81-298-38-8674)

FEATURES

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source
1. .181
/organism="Sus scrofa domestica"
/mol_type="genomic DNA"
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/clone_lib="Swine genomic BAC library, National Institute
of Agrobiological Resources, Ibaraki, Japan"
/notes="synonym:Sus scrofa domestica"
1. .181
/standard_name="346D10R"

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1. .20
/PCR_conditions="denaturation 30s at 95 degrees, annealing
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elongation 5min at 72 degrees, 40 cycles"
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ORIGIN

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	Best Local Similarity	55.6%;	Pred. No. 1.1e+04;		
	Matches	30;	Conservative	4;	Mismatches 20; Indels 0; Gaps 0;
QY	1	GGGAGAGAGAAAGAGGAUGGGGACUAUACCGGUAUCGUGCCUCCAUUC	54		
Db	94	GTGTGTGGGGAGAGGCTGGGGAGACAGACTGAATAGCGTGGATGTCAAGCC	41		

1 GGGAGAGAGGAAGAGGGATGGGACTTATACCGGGTAAATGCTGGCTCCCAATTC 54

[illegible]

RESULT 7

AU046875/c	AU046875	187 bp	DNA	linear	STS 22-APR-1999
LOCUS	Rattus norvegicus, OTSUKA clone, 085b01, microsatellite sequence, sequence tagged site.				
DEFINITION					
ACCESSION	AU046875				
VERSION	AU046875.1	GI:4631510			
KEYWORDS	STS.				
SOURCE	Rattus norvegicus (Norway rat)				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (sites)				
AUTHORS	Watanabe, T.K., Hishigaki, H., Okuno, S., Mizoguchi, A., Oga, K., Tsuji, A., Ono, T., Yamasaki, Y., Kanemoto, N., Takahashi, E., Irie, Y., Nakamura, Y., Takagi, Y. and Tanigami, A.				
TITLE	The large-scale mapping of rat microsatellite markers				

REFERENCES

AUTHORS
Watanabe, T. K.
TITLE
Direct Submission
JOURNAL
Submitted (11-DEC-1998) Takeshi K Watanabe, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10, Kagasuno, Kawachi-cho, Tokushima, Tokushima 771-0192, Japan
(E-mail: watanabe@otsuka.gr.jp; Tel: +81-886-65-2888, Fax: +81-886-37-1035)

FEATURES

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1. .187
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="Brown Norway"
/db_xref="taxon:10116"
/clone="085b01"
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Best Local Similarity	51.9%;	Pred. No. 1.1e+04;		

	Matches	28; Conservative	6; Mismatches	20; Indels	0; Gaps	0;
Qy	1	GGGAGAGAGGAACAGCGAUGGGGCUAUACCGGUAAGUGGUGCUCCCAUUC	54			
	62	GGGAGGGGAGGAGAGAGATTTATCCATAAAGTCTCCCTCGTCTAC	9			
Db						

RESULT 8

AR141692	AR141692	108 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	Sequence 3	from patent US 6,146,886.			
DEFINITION	AR141692				
ACCESSION	AR141692.1	GI:15101208			
VERSION					

SOURCE

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 108)
TITLE	Thompson, J. D.
JOURNAL	RNA polymerase III-based expression of therapeutic RNAs
FEATURES	Patent: US 6146895-A 3 14-NOV-2000; Location/Qualifiers 1..108 source

ORIGIN

Query Match	22.7%	Score 21.8;	DB 6;	Length 108;
Best Local Similarity	52.3%;	Pred. No. 1.3e+04;		
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Dd 7 ACAGCAGAGTCGGCAGCGGAAGCTGCTGGCCCATTAACCCAGAGGTCGATGGATCGAA 66

Qv 89 AIICCC 93

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RESIST. 9

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PREFERENCE

REFERENCE	AUTHORS	TITLE
Stinchcomb, D. T., Dudycz, L. W., Chowrira, B., Grimm, S., Dizenzo, A., Karpelsky, A., Draper, K. G., Kisch, K., Matulich-Adamic, J., Mcswigley, J. A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S. M., Sweedler, D., Thompson, J. D., Tracz, D., Usman, N., Wincott, F. E. and Woolf, T.		Method and reagent for inhibiting the expression of disease related genes

JOURNAL

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FEATURES
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Best Local Similarity	52.3%;	Pred. No. 1.3e+04;		
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Db 7 ACAGCAGAGTGGCGCAGCGGAAGCGTGTCTGGGCCCCATAACCCAGAGGTCGATGGATCGAA 66

QY 89 AUCCC 93
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Db 67 ACCCC 71

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LOCUS ARI141696 109 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6146886.
ACCESSION ARI141696
VERSION ARI141696.1 GI:15101212
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 109)
AUTHORS Thompson,J.D.
TITLE RNA polymerase III-based expression of therapeutic RNAs
JOURNAL Patent: US 6146886-A 7 14-NOV-2000;
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/mol_type="unassigned DNA"

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Best Local Similarity 52.3%; Pred. No. 1.3e+04;
Matches 34; Conservative 4; Mismatches 27; Indels 0; Gaps 0;

QY 29 ACCGCGUAUUGCUGCCUCCCAUUCGCGAAGCGTGTCTGGGCCCCATAACCCAGAGGTCGATGGATCGAA 88

Db 7 ACAGCAGAGTGGCGCAGCGGAAGCGTGTCTGGGCCCCATAACCCAGAGGTCGATGGATCGAA 66

QY 89 AUCCC 93
| | | |

Db 67 ACCCC 71

RESULT 11
AX638754
LOCUS AX638754 109 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 5893 from Patent EP1260586.
ACCESSION AX638754
VERSION AX638754.1 GI:28474368
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Dorenzo,A., Karpisisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J., Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Wolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 5893 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
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QY 29 ACCGCGUAUUGCUGCCUCCCAUUCGCGAAGCGTGTCTGGGCCCCATAACCCAGAGGTCGATGGATCGAA 88

Db 7 ACAGCAGAGTGGCGCAGCGGAAGCGTGTCTGGGCCCCATAACCCAGAGGTCGATGGATCGAA 66

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QY 89 AUCCC 93
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Db 67 ACCCC 71

RESULT 12
ARI141694
LOCUS ARI141694 133 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6146886.
ACCESSION ARI141694
VERSION ARI141694.1 GI:15101210
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 133)
AUTHORS Thompson,J.D.
TITLE RNA polymerase III-based expression of therapeutic RNAs
JOURNAL Patent: US 6146886-A 5 14-NOV-2000;
FEATURES Location/Qualifiers
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source /organism="unknown"
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QY 89 AUCCC 93
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Db 67 ACCCC 71

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ARI141698
LOCUS ARI141698 133 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6146886.
ACCESSION ARI141698
VERSION ARI141698.1 GI:15101214
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 133)
AUTHORS Thompson,J.D.
TITLE RNA polymerase III-based expression of therapeutic RNAs
JOURNAL Patent: US 6146886-A 9 14-NOV-2000;
FEATURES Location/Qualifiers
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source /organism="unknown"
/mol_type="unassigned DNA"

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Db 7 ACAGCAGAGTGGCGCAGCGGAAGCGTGTCTGGGCCCCATAACCCAGAGGTCGATGGATCGAA 66

QY 89 AUCCC 93
| | | |

Db 67 ACCCC 71

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 01:39:24 ; Search time 341.082 Seconds
(without alignments)
1195.685 Million cell updates/sec

Title: US-09-963-827B-3
Perfect score: 96
Sequence: 1 gggagagaggaagggaug.....cgaugacuaggaucacccc 96

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 3774412

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s:*
2: Geneseqn1990s:*
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10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	62	64.6	94	6	ABN88506 Coagulati
3	60.8	63.3	96	6	ABN88504 Coagulati
4	60	62.5	95	6	ABN88509 Coagulati
5	59.2	61.7	96	6	ABN88489 Coagulati
6	58.4	60.8	95	6	ABN88499 Coagulati
7	58.4	60.8	95	6	ABN88491 Coagulati
8	56	58.3	96	6	ABN88497 Coagulati
9	56	58.3	96	6	ABN88500 Coagulati
10	55	57.3	96	6	ABN88502 Coagulati
11	54.4	56.7	96	6	ABN88527 Coagulati
12	52.8	55.0	96	6	ABN88521 Coagulati
13	51.2	53.3	96	6	ABN88510 Coagulati
14	50.8	52.9	96	6	ABN88498 Coagulati
15	49.6	51.7	96	6	ABN88501 Coagulati
16	49.6	51.7	96	6	ABN88496 Coagulati
17	49.6	51.7	96	6	ABN88503 Coagulati
18	49.6	51.7	96	6	ABN88493 Coagulati
19	49.6	51.7	96	6	ABN88531 Coagulati
20	49.6	51.7	96	6	ABN88528 Coagulati
21	49.6	51.7	96	6	ABN88526 Coagulati
22	48	50.0	96	6	ABN88529 Coagulati
23	48	50.0	96	6	ABN88508 Coagulati

ALIGNMENTS

RESULT 1

ABN88490
ID ABN88490 standard; RNA; 96 BP.
XX
AC ABN88490;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:3.
XX
KW RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
DR WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
family members, Ang1 or Ang2, useful for modulating coagulation pathway
factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1A; 216pp; English.
XX
CC The present invention describes RNA aptamers (I, II, III) that selectively
bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
a dissociation constant for the coagulation pathway factor, an E2F family
member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) are
cardiant and cytostatic activities. (I) are useful for modulating the
biological activity of a coagulation pathway factor which involves
administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that

24	48	50.0	96	6	ABN88530	Coagulati
25	47.2	49.2	92	6	ABN88559	Coagulati
26	47.2	49.2	95	6	ABN88507	Coagulati
27	47.2	49.2	95	6	ABN88515	Coagulati
28	46.6	48.5	97	6	ABN88511	Coagulati
29	46.4	48.3	96	6	ABN88533	Coagulati
30	46.4	48.3	96	6	ABN88492	Coagulati
31	46.4	48.3	96	6	ABN88532	Coagulati
32	46.4	48.3	96	6	ABN88534	Coagulati
33	46.4	48.3	96	6	ABN88505	Coagulati
34	46.2	48.1	99	6	ABN88518	Coagulati
35	45	46.9	97	6	ABN88523	Coagulati
36	45	46.9	97	6	ABN88514	Coagulati
37	44.8	46.7	92	6	ABN88494	Coagulati
38	43.4	45.2	92	6	ABN88512	Coagulati
39	43.4	45.2	97	6	ABN88519	Coagulati
40	43.2	45.0	96	6	ABN88488	Coagulati
41	41.8	43.5	97	6	ABN88516	Coagulati
42	41.8	43.5	97	6	ABN88513	Coagulati
43	40.4	42.1	100	6	ABN88520	Coagulati
44	40.2	41.9	97	6	ABN88524	Coagulati
45	40	41.7	40	7	ABZ21242	FIXa apta

PI Sullenger BA, Rusconi CP;
XX
XX WPI; 2002-479560/51.
XX
XX Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
XX Claim 13; Fig 1B; 216pp; English.
XX
XX The present invention describes RNA aptamers (I, II, III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiotensin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic,
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABN81231 represent
CC sequences used in the exemplification of the present invention
XX
XX SQ Sequence 95 BP; 25 A; 27 C; 28 G; 0 T; 15 U; 0 Other;

Query Match 62.5%; Score 60; DB 6; Length 95;
Best Local Similarity 83.3%; Pred. No. 4e-12;
Matches 80; Conservative 0; Mismatches 15; Indels 1; Gaps 1

Qy 1 GCGAGAGAGGAAGGAGGGAACUAUACCGGUAUUGCUGCCUCCCAUUCGGAACG 60
Db 1 GCGAGAGAGGAAGGAGGGAUGGGCGCCAUU -CGCACAUUGCUGCAUCGCGCCGUAAGA 59

Qy 61 CUCAUAUACCCAGAGGUGCAUAGUACUGAUCCGCCCC 96
Db 60 ACCAUUACCCAGAGGUGCAUAGUACUGAUCCGCCCC 95

RESULT 5
ABN88489
ID ABN88489 standard; RNA; 96 BP.
XX
XX AC ABN88489;
XX
XX XX
DT 19-AUG-2002 (first entry)
XX
XX Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:2.
XX
XX RNA aptamer; identification; coagulation factor; angiotensin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200226932-A2.
PN
XX
XX 04-APR-2002.
PD
XX

they specifically bind, and for identifying substances to which they

CC plasma or the activation of platelets in response to thrombin. (II) are anticoagulants and significantly delay the clotting time of normal human

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OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 02:54:20 ; Search time 78.6824 Seconds
(without alignments)
677.093 Million cell updates/sec

Title: US-09-963-827B-3

Perfect score: 96

Sequence: 1 gggagagaggaggaggagg.....cgauagucaggaucccccc 96

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 979464

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/2/ina/5A COMB.seq.*

2: /cgn2_6/prodata/2/ina/5B COMB.seq.*

3: /cgn2_6/prodata/2/ina/6A COMB.seq.*

4: /cgn2_6/prodata/2/ina/6B COMB.seq.*

5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*

6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.6	24.6	87	5	PCT-US95-05600-12
2	21.8	22.7	108	3	US-08-512-861A-3
3	21.8	22.7	109	3	US-08-512-861A-7
4	21.8	22.7	133	3	US-08-512-861A-5
5	21.8	22.7	133	3	US-08-512-861A-9
6	21.8	22.7	146	3	US-08-512-861A-4
7	21.8	22.7	146	3	US-08-512-861A-8
8	21.8	22.7	171	3	US-08-512-861A-6
9	21.8	22.7	171	3	US-08-512-861A-10
10	21.4	22.3	107	4	US-09-581-617-1
11	21.2	22.1	176	4	US-09-919-172-11
12	20.6	21.5	88	3	US-08-512-861A-1
13	20.6	21.5	129	3	US-08-512-861A-13
14	20.6	21.5	167	3	US-08-512-861A-14
15	20.4	21.2	180	1	US-08-443-640-4
16	19.8	20.6	70	3	US-08-512-861A-2
17	19.8	20.6	112	3	US-08-512-861A-15
18	19.8	20.6	112	3	US-08-512-861A-16
19	19.8	20.6	148	3	US-08-512-861A-17
20	19.8	20.6	168	3	US-08-512-861A-18
21	19.6	20.4	131	4	US-08-879-337-11
22	19.6	20.4	193	2	US-08-481-658B-40
23	19.6	20.4	193	2	US-08-477-504A-40
24	19.6	20.4	193	2	US-08-486-756A-40
25	19.6	20.4	193	2	US-08-485-862B-40
26	19.6	20.4	193	3	US-08-787-739-40
27	19.6	20.4	193	3	US-08-487-077A-40

c	28	19.6	20.4	193	3	US-08-485-863A-40	Sequence 40, Appl
c	29	19.6	20.4	193	3	US-08-485-049D-40	Sequence 40, Appl
c	30	19.6	20.4	193	3	US-09-178-115-40	Sequence 40, Appl
c	31	19.6	20.4	193	3	US-09-177-776-40	Sequence 40, Appl
c	32	19.4	20.2	82	5	PCT-US95-05600-14	Sequence 14, Appl
c	33	19.4	20.2	87	5	PCT-US95-05600-11	Sequence 11, Appl
c	34	19.2	20.0	79	5	PCT-US95-05600-13	Sequence 13, Appl
c	35	18.8	19.6	84	2	US-08-488-402A-97	Sequence 97, Appl
c	36	18.8	19.6	84	2	US-08-484-552A-97	Sequence 97, Appl
c	37	18.8	19.6	84	5	PCT-US96-09472-97	Sequence 97, Appl
c	38	18.8	19.6	114	4	US-09-494-921-11	Sequence 11, Appl
c	39	18.8	19.6	117	1	US-08-403-762A-94	Sequence 94, Appl
c	40	18.4	19.2	28	5	PCT-US95-05600-3	Sequence 3, Appl
c	41	18.4	19.2	68	5	PCT-US95-05600-15	Sequence 15, Appl
c	42	18.4	19.2	70	5	PCT-US95-05600-9	Sequence 9, Appl
c	43	18.4	19.2	70	5	PCT-US95-05600-10	Sequence 10, Appl
c	44	18.4	19.2	71	5	PCT-US95-05600-7	Sequence 7, Appl
c	45	18.4	19.2	72	5	PCT-US95-05600-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
PCT-US95-05600-12
; Sequence 12, Application PC/TUS9505600
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: NEUWLANDT, DAN
; APPLICANT: WECKER, MATTHEW
; APPLICANT: SCHNEIDER, DANIEL J.
; APPLICANT: FEIGON, JULI
; APPLICANT: ALLEN, PATRICK
; APPLICANT: SULLENGER, BRUCE A.
; APPLICANT: DOUDNA, JENNIFER A.
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
; TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
; TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C. 200
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05600
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,863
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,632
FILING DATE: 24-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 09-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361,795
FILING DATE: 21-DECEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 08-SEPTEMBER-1993
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX17/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; PCT-US95-05600-12

Query Match 24.6%; Score 23.6; DB 5; Length 87;
Best Local Similarity 63.1%; Pred. No. 7.8; Indels 2; Gaps 1;
Matches 53; Conservative 0; Mismatches 29;

QY 1 GGGAGAGGAGGAGGAGGAGGAGGAC--UAUACCGGUAUUGUGCGUCCGCCCAUUCGGAA 58
Db 1 GGGAGAGGAGGAGGUGUGUGGCGGCCGUGGAGACAUAGAGGUCAACUGAAUUGUCA 60

QY 59 CCUCAUAACCCAGAGGUGGUAUG 82
Db 61 CGAGCAUAACCCAGAGGUGGUAUG 84

RESULT 2
US-08-512-861A-3
; Sequence 3, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512,861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886member 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109
; TYPE: nucleic acid
; STRANDEDNESS: single
; FILING DATE: No. 6146886member 10, 1994

; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-512-861A-3

Query Match 22.7%; Score 21.8; DB 3; Length 108;
Best Local Similarity 58.5%; Pred. No. 40;
Matches 38; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 29 ACCCGUAUUGUGCGUCCUCCCAUUCGGAAACCGUAUACCCAGAGGUGGUAUACUGG 88
Db 7 ACAGCAGAGUGGCGCAGCGGAAGCGUGUGGCGCCCAUAAACCCAGAGGUGGUAUACGAA 66

QY 89 AUCCC 93
Db 67 ACCCC 71

RESULT 3
US-08-512-861A-7
; Sequence 7, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512,861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886member 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109
; TYPE: nucleic acid
; STRANDEDNESS: single
; FILING DATE: No. 6146886member 10, 1994
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TOPOLOGY: linear
US-08-512-861A-7

Query Match 22.7%; Score 21.8; DB 3; Length 109;
Best Local Similarity 58.5%; Pred. No. 41; Mismatches 0; Gaps 0;
Matches 38; Conservative 0; Indels 27; Indels 0; Gaps 0;
QY 29 ACCGCGUAUUGCUGCCUCCCAUUCGCGAAACGCUCAUAACCCAGAGGUGCAUAGUACUGG 88
DB 7 ACAGCAGAGUGGCGCGACGCGAAGCGUGCGGCCCAUAACCCAGAGGUGCAUAGUACUGG 66
QY 89 AUCCC 93
DB 67 ACCCC 71

RESULT 4

US-08-512-861A-5
; Sequence 5, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512,861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA: Two
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886ember 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-512-861A-5

Query Match 22.7%; Score 21.8; DB 3; Length 133;
Best Local Similarity 58.5%; Pred. No. 43; Mismatches 0; Gaps 0;
Matches 38; Conservative 0; Indels 27; Indels 0; Gaps 0;
QY 29 ACCGCGUAUUGCUGCCUCCCAUUCGCGAAACGCUCAUAACCCAGAGGUGCAUAGUACUGG 88
DB 7 ACAGCAGAGUGGCGCGACGCGAAGCGUGCGGCCCAUAACCCAGAGGUGCAUAGUACUGG 66
QY 89 AUCCC 93
DB 67 ACCCC 71

Db 67 ACCCC 71

RESULT 5

US-08-512-861A-9
; Sequence 9, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/512,861A
; FILING DATE: August 8, 1995
; PRIOR APPLICATION DATA: Two
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886ember 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-512-861A-9

Query Match 22.7%; Score 21.8; DB 3; Length 133;
Best Local Similarity 58.5%; Pred. No. 43; Mismatches 0; Gaps 0;
Matches 38; Conservative 0; Indels 27; Indels 0; Gaps 0;
QY 29 ACCGCGUAUUGCUGCCUCCCAUUCGCGAAACGCUCAUAACCCAGAGGUGCAUAGUACUGG 88
DB 7 ACAGCAGAGUGGCGCGACGCGAAGCGUGCGGCCCAUAACCCAGAGGUGCAUAGUACUGG 66
QY 89 AUCCC 93
DB 67 ACCCC 71

RESULT 6

US-08-512-861A-4
; Sequence 4, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 8, 1995
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886ember 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; Query Match 22.7%; Score 21.8; DB 3; Length 146;
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; QY 89 AUCCC 93
; DB 67 ACCCC 71
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; RESULT 7
; US-08-512-861A-8
; Sequence 8, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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; FILING DATE: August 8, 1995
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886ember 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
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; RESULT 7
; US-08-512-861A-8
; Sequence 8, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
; NUMBER OF SEQUENCES: 25
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; STATE: California
; COUNTRY: U.S.A.
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; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886ember 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
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; TELEFAX: (213) 955-0440
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; QY 89 AUCCC 93
; DB 67 ACCCC 71
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; RESULT 7
; US-08-512-861A-8
; Sequence 8, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
; NUMBER OF SEQUENCES: 25
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; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
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; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886ember 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
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; TELEFAX: (213) 955-0440
; TELEX: 67-3510
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; TOPOLOGY: linear
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; US-08-512-861A-4
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; Query Match 22.7%; Score 21.8; DB 3; Length 146;
; Best Local Similarity 58.5%; Pred. No. 45;
; Matches 38; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
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; DB 7 ACAGCAGAGUGGCGGCGAGCGGAGCGUGGCGGCCCAUAACCCAGAGGUGCAUAGUACUGG 66
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; QY 89 AUCCC 93
; DB 67 ACCCC 71
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; RESULT 7
; US-08-512-861A-8
; Sequence 8, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
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; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 8, 1995
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886ember 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
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; Best Local Similarity 58.5%; Pred. No. 45;
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; QY 89 AUCCC 93
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; RESULT 7
; US-08-512-861A-8
; Sequence 8, Application US/08512861A
; Patent No. 6146886
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
; TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 8, 1995
; APPLICATION NUMBER: 08/293,520
; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886ember 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
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; TYPE: nucleic acid
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; TOPOLOGY: linear
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; US-08-512-861A-4
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; Query Match 22.7%; Score 21.8; DB 3; Length 146;
; Best Local Similarity 58.5%; Pred. No. 45;
; Matches 38; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
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; QY
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 171
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-512-861A-6

Query Match 22.7%; Score 21.8; DB 3; Length 171;
Best Local Similarity 58.5%; Pred. No. 47;
Matches 38; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 29 ACCGCGUAUUGUGUGCCUCCCAUCCGGAACGCUCAUAACCCAGAGUCCGAUAGUACUGG 88
DB 7 ACAGCAGAGUGGCGCAGCGGAGGUGUGGCGCCCAUAACCCAGAGUCCGAUAGUACUGG 66
QY 89 AUCCC 93
DB 67 ACCCC 71

RESULT 9

US-08-512-861A-10
Sequence 10, Application US/08512861A
Patent No. 6146886

GENERAL INFORMATION:
APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAs
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
PRIOR APPLICATION DATA: Two
APPLICATION NUMBER: 08/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6146886 member 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 215/154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 171
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-512-861A-10

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Best Local Similarity 58.5%; Pred. No. 47;

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QY 89 AUCCC 93
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RESULT 10

US-09-581-617-1
Sequence 1, Application US/09581617
Patent No. 6346385

GENERAL INFORMATION:
APPLICANT: Teijin Limited
TITLE OF INVENTION: Analysis of predisposition based on human airway
TITLE OF INVENTION: trypsin protease gene polymorphism
FILE REFERENCE: Q59572
CURRENT APPLICATION NUMBER: US/09/581,617
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: PCT/JP98/05689
PRIOR FILING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: 9-346494 JAPAN
PRIOR FILING DATE: 1997-12-16
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 107
TYPE: DNA
ORGANISM: Homo sapiens
US-09-581-617-1

Query Match 22.3%; Score 21.4; DB 4; Length 107;

Best Local Similarity 50.9%; Pred. No. 57;

Matches 28; Conservative 6; Mismatches 21; Indels 0; Gaps 0;
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DB 13 CTACCTACCCATCTGGGAACAATTAGATAGACGTCAATGAGACTGCACCCCTC 67

RESULT 11

US-09-919-172-11
Sequence 11, Application US/09919172
Patent No. 6673545

GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
SEQ ID NO 11
LENGTH: 176
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673545 378497.1
NAME/KEY: unsure
LOCATION: 18, 30, 35, 39, 44, 52, 87, 93, 108, 112, 114, 151, 166, 168, 170
OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-11

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; FILING DATE: August 19, 1994
; APPLICATION NUMBER: 08/337,608
; FILING DATE: No. 6146886member 10, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 215/154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
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QY 89 AUCCCC 95
Db 67 ACCAUC 73

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RESULT 15
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; Patent No. 5691140
; GENERAL INFORMATION:
; APPLICANT: NOREN, CHRISTOPHER J.
; APPLICANT: EVANS, PAUL D.
; TITLE OF INVENTION: BIDIRECTIONAL IN VITRO TRANSCRIPTION
; TITLE OF INVENTION: VECTORS UTILIZING A SINGLE RNA POLYMERASE FOR BOTH
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEW ENGLAND BIOLABS, INC
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/443,640
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.

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; REFERENCE/DOCKET NUMBER: NEB-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 4:
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GenCore version 5.1.6
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Maximum DB seq length: 200
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Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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3	63.3	60.8	95	10	US-09-963-827B-17	Sequence 17, Appl	Sequence 17, Appl
4	60	62.5	95	10	US-09-963-827B-22	Sequence 22, Appl	Sequence 22, Appl
5	59.2	61.7	96	10	US-09-963-827B-2	Sequence 2, Appl	Sequence 2, Appl
6	58.4	60.8	95	10	US-09-963-827B-4	Sequence 4, Appl	Sequence 4, Appl
7	59.4	60.8	95	10	US-09-963-827B-12	Sequence 12, Appl	Sequence 12, Appl
8	56	58.3	96	10	US-09-963-827B-10	Sequence 10, Appl	Sequence 10, Appl
9	56	58.3	96	10	US-09-963-827B-13	Sequence 13, Appl	Sequence 13, Appl
10	55	57.3	96	10	US-09-963-827B-15	Sequence 15, Appl	Sequence 15, Appl
11	54.4	56.7	96	10	US-09-963-827B-40	Sequence 40, Appl	Sequence 40, Appl
12	51.2	53.1	96	10	US-09-963-827B-23	Sequence 23, Appl	Sequence 23, Appl
13	50.8	52.9	96	10	US-09-963-827B-11	Sequence 11, Appl	Sequence 11, Appl
14	49.6	51.7	96	10	US-09-963-827B-6	Sequence 6, Appl	Sequence 6, Appl
15	49.6	51.7	96	10	US-09-963-827B-9	Sequence 9, Appl	Sequence 9, Appl

ALIGNMENTS

RESULT 1

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US-09-963-827B-3
; Sequence 3, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Sullenger, Bruce
; APPLICANT: Rusconi, Christopher
; TITLE OF INVENTION: RNA APAMERS AND METHODS FOR IDENTIFYING THE SAME
; FILE REFERENCE: 180/124/2
; CURRENT APPLICATION NUMBER: US/09/963,827B
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,654
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.0

```

Query Match	100.0%:	Score 96:	DB 10:	Length 96:
-------------	---------	-----------	--------	------------

Query Match	Score 50, SS 10, Mengen 50,	Indels	Gaps
Best Local Similarity	100.0%; Pred. No. 1.5e+26;	0	0
Best Match	100.0%;	0	0
Matches	95: Conservative	Mismatches	0

Qy 1 GGGAGAGAGAAAGAGGGAUGGGGACUUAACCGCGUAUUGCUCGCCCAUCCGGAACG 60
Db 1 GGGAGAGAGAGAGGGAUGGGGACUUAACCGCGUAUUGCUCGCCCAUCCGGAACG 60			
Qy 61 CUUAUACCAGAGGVCGAUAGUACVUGAUCCCCCC 96


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; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,654
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 95
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RNA aptamer
; NAME/KEY: misc feature
; LOCATION: (1)..(95)
; OTHER INFORMATION: RNA aptamer
US-09-963-827B-12

Query Match          60.8%; Score 58.4; DB 10; Length 95;
Best Local Similarity 82.3%; Pred. No. 2.7e-12;
Matches 79; Conservative 0; Mismatches 16; Indels 1; Gaps 0;

Qy 1 GGGAGAGAGGAAGAGGAGGACUAUACCGGCUAAUGCGCUCUCCCAUUCGGAACG 60
Db 1 GGGAGAGAGGAAGAGGAGGACUAUA-CGUGAACGACUGCAUCCACUUCUCCCGCAU 59

Qy 61 CUCAUAACCCAGAGGUGCGUAUAGUACUGGAUCCUCCCC 96
Db 60 GGCAUAACCCAGAGGUGCGUAUAGUACUGGAUCCUCCCC 95

RESULT 8
US-09-963-827B-10
; Sequence 10, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Sullenger, Bruce
; APPLICANT: Rusconi, Christopher
; TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
; FILE REFERENCE: 180/124/2
; CURRENT APPLICATION NUMBER: US/09/963,827B
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,654
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 96
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RNA aptamer
; NAME/KEY: misc feature
; LOCATION: (1)..(96)
; OTHER INFORMATION: RNA aptamer
US-09-963-827B-10

Query Match          58.3%; Score 56; DB 10; Length 96;
Best Local Similarity 74.0%; Pred. No. 2.2e-11;
Matches 71; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

Qy 1 GGGAGAGAGGAAGAGGAGGACUAUACCGGCUAAUGCGCUCUCCCAUUCGGAACG 60
Db 1 GGGAGAGAGGAAGAGGAGGACUAUAACAUUGGUGAUCCACCCACAUGAACCAC 60

Qy 61 CUCAUAACCCAGAGGUGCGUAUAGUACUGGAUCCUCCCC 96
Db 61 AGCAUAACCCAGAGGUGCGUAUAGUACUGGAUCCUCCCC 96

RESULT 9
US-09-963-827B-13

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Search completed: April 9, 2004, 10:11:30
Job time : 1190.14 secs

Result No.	Score	Query		DB	ID	Description
		Match	%			
C 1	20.2	21.0	175	5	US-09-969-034-110	Sequence 110, App
C 2	19.8	20.6	185	6	US-10-793-479-28742	Sequence 28742, App
C 3	19.8	20.6	185	6	US-10-793-479-28742	Sequence 13386, App
C 4	19.6	20.4	174	6	US-10-793-479-8881	Sequence 8881, App
C 5	19.4	20.2	155	6	US-10-803-180-1481	Sequence 1481, App
C 6	19.4	20.2	155	6	US-10-803-180-1490	Sequence 1490, App
C 7	19.4	20.2	156	6	US-10-803-180-1472	Sequence 1472, App
C 8	19.4	20.2	182	6	US-10-803-180-1488	Sequence 1488, App
C 9	19.4	20.2	182	6	US-10-803-180-1496	Sequence 1496, App
C 10	19.4	20.2	183	6	US-10-803-180-1479	Sequence 1479, App
C 11	19.2	20.0	51	6	US-10-785-782-6107	Sequence 6107, App
C 12	19.2	20.0	160	6	US-10-793-479-10298	Sequence 10298, App
C 13	19	19.8	51	6	US-10-785-782-8362	Sequence 8362, App
C 14	19	19.8	170	6	US-10-793-479-33426	Sequence 33426, App
C 15	19	19.8	194	6	US-10-803-180-1484	Sequence 1484, App
C 16	19	19.8	194	6	US-10-803-180-1493	Sequence 1493, App
C 17	19	19.8	195	6	US-10-803-180-1475	Sequence 1475, App
C 18	18.8	19.6	178	6	US-10-767-701-19121	Sequence 19121, App
C 19	18.6	19.4	51	6	US-10-785-782-23966	Sequence 23966, App
C 20	18.6	19.4	101	6	US-10-708-204-7187	Sequence 7187, App
C 21	18.6	19.4	139	6	US-10-793-479-24132	Sequence 24132, App
C 22	18.6	19.4	175	6	US-10-793-479-14465	Sequence 14465, App
C 23	18.6	19.4	183	6	US-10-793-479-16584	Sequence 16584, App
C 24	18.4	19.2	145	6	US-10-793-479-23541	Sequence 23541, App
C 25	18.2	19.0	51	6	US-10-785-782-3679	Sequence 3679, App
C 26	18.2	19.0	79	6	US-10-708-951-54485	Sequence 54485, App

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; CURRENT APPLICATION NUMBER: US/10/793,479
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US/09/513,999
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8881
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 12
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 13
; OTHER INFORMATION: m=a or c
;
US-10-793-479-8881

Query Match      20.4%; Score 19.6; DB 6; Length 174;
Best Local Similarity 57.1%; Pred.No. 3.4e+02;
Matches 24; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY      46  CCCCAUCCGGAACGCUCAUAACCCAGAGGUCGAUAGUACUG 87
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      73  CCTTTTCCAGAACACTCAAAACCTCATGACCAAGAGTACAG 32

RESULT 5
US-10-803-180-1481/c
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001511
; CURRENT APPLICATION NUMBER: US/10/803,180
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1481
; LENGTH: 155
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-10-803-180-1481

Query Match      20.2%; Score 19.4; DB 6; Length 155;
Best Local Similarity 55.6%; Pred.No. 3.9e+02;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY      35  UAAUGUCGUCUCCCAUUCGGAACGCUCAUAACCCAGAGGUCGA 79
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      68  TAAAGGTTTAAACCCCAATCCCAAGTGCTGAAAAACCCAGAGGCTGA 24

RESULT 6
US-10-803-180-1490/c
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001511
; CURRENT APPLICATION NUMBER: US/10/803,180
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1490
; LENGTH: 155
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-803-180-1490

Query Match          20.2%; Score 19.4; DB 6; Length 155;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 35 UAAUGCUGCCUCCCAUUCGGAACGCUCAUAACCCAGAGGUGCA 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 68 TAAAGGTTTAAACCCCAATCCCAAGTCTGAAAAAACAGAGGCTGA 24

RESULT 7
US-10-803-180-1472/c
; Sequence 1472, Application US/10803180
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001511
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1472
; LENGTH: 156
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-180-1472

Query Match          20.2%; Score 19.4; DB 6; Length 156;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 35 UAAUGCUGCCUCCCAUUCGGAACGCUCAUAACCCAGAGGUGCA 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||
Db 68 TAAAGGTTTAAACCCCAATCCCAAGTCTGAAAAAACAGAGGCTGA 24

RESULT 8
US-10-803-180-1488/c
; Sequence 1488, Application US/10803180
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001511
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1488
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-180-1488

Query Match          20.2%; Score 19.4; DB 6; Length 182;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 35 UAAUGCUGCCUCCCAUUCGGAACGCUCAUAACCCAGAGGUGCA 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||
Db 95 TAAAGGTTTAAACCCCAATCCCAAGTCTGAAAAAACAGAGGCTGA 51

RESULT 9
US-10-803-180-1496/c
; Sequence 1496, Application US/10803180
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001511
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1496
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-180-1496

Query Match          20.2%; Score 19.4; DB 6; Length 182;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 35 UAAUGCUGCCUCCCAUUCGGAACGCUCAUAACCCAGAGGUGCA 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||
Db 95 TAAAGGTTTAAACCCCAATCCCAAGTCTGAAAAAACAGAGGCTGA 51

RESULT 10
US-10-803-180-1479/c
; Sequence 1479, Application US/10803180
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001511
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1479
; LENGTH: 183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-180-1479

Query Match          20.2%; Score 19.4; DB 6; Length 183;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 35 UAAUGCUGCCUCCCAUUCGGAACGCUCAUAACCCAGAGGUGCA 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||
Db 95 TAAAGGTTTAAACCCCAATCCCAAGTCTGAAAAAACAGAGGCTGA 51

RESULT 11
US-10-785-782-6107/c
; Sequence 6107, Application US/10785782
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Meti
; FILE REFERENCE: 15966-611
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US/09/755,374
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/174962
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 6107
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (26)...(0)
; OTHER INFORMATION: 1 of 2 allelic variants (6108 is other entry)
; FEATURE:
; NAME/KEY: misc_feature
```

```
; FILE REFERENCE: CL001511
; CURRENT APPLICATION NUMBER: US/10/803,180
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1496
; LENGTH: 182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-180-1496

Query Match          20.2%; Score 19.4; DB 6; Length 182;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 35 UAAUGCUGCCUCCCAUUCGGAACGCUCAUAACCCAGAGGUGCA 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||
Db 95 TAAAGGTTTAAACCCCAATCCCAAGTCTGAAAAAACAGAGGCTGA 51

RESULT 10
US-10-803-180-1479/c
; Sequence 1479, Application US/10803180
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001511
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1479
; LENGTH: 183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-180-1479

Query Match          20.2%; Score 19.4; DB 6; Length 183;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 35 UAAUGCUGCCUCCCAUUCGGAACGCUCAUAACCCAGAGGUGCA 79
   :|||:|||||:|||||:|||||:|||||:|||||:|||||
Db 95 TAAAGGTTTAAACCCCAATCCCAAGTCTGAAAAAACAGAGGCTGA 51

RESULT 11
US-10-785-782-6107/c
; Sequence 6107, Application US/10785782
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Meti
; FILE REFERENCE: 15966-611
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US/09/755,374
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/174962
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 6107
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (26)...(0)
; OTHER INFORMATION: 1 of 2 allelic variants (6108 is other entry)
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43986469
US-10-785-782-6107

Query Match          20.0%; Score 19.2; DB 6; Length 51;
Best Local Similarity 52.5%; Pred.No. 3.3e+02;
Matches 21; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY   15  GGGAUGGGGACUUAACCAGCGGUAAUGCUCGCCAUCC 54
      ||||| :||| :||| :||| :||| :||| :||| :|||
DB    40  GTGAAGGGGTGTATGAGTGATCTTCGC GCCCCCCCTCCC 1

RESULT 12
US-10-793-479-10298
; Sequence 10298, Application US/10793479
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/10/793,479
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US/09/513,999
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10298
; LENGTH: 160
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 41
; OTHER INFORMATION: s=g or c
US-10-793-479-10298

Query Match          20.0%; Score 19.2; DB 6; Length 160;
Best Local Similarity 53.6%; Pred.No. 4.7e+02;
Matches 30; Conservative 3; Mismatches 23; Indels 0; Gaps 0;

QY   1  GCGAGAGGAGAAGGAGGAGGAGCUAUGC CGUAAUGCUCGCCAUCCGG 56
      ||||||| :||| :||| :||| :||| :||| :||| :|||
DB    81  GAGTGAAGAGAAGGAGGAGTAGGGTCTCC TCTGAGTAGCTGGACTACAGGCCCG 136

RESULT 13
US-10-785-782-8362
; Sequence 8362, Application US/10785782
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide Polymorphisms and Meth
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 15966-611
; CURRENT APPLICATION NUMBER: US/10/785,782
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US/09/755,374
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/174962
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 28742
; SEQ ID NO 8362
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (26)...(0)
; OTHER INFORMATION: 2 of 2 allelic variants (8361 is other entry)
```

```

;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43955877
US-10-785-782-8362

Query Match          19.8%; Score 19; DB 6; Length 51;
Best Local Similarity 60.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      61  CUCAUAAACCAGAGGUCGUAAGUACUGGAGUCCGCC 95
DB      10  CTATAAACCTGAGGTCGAAAGCTCTGGATAGTC 44

RESULT 14
US-10-793-479-33426/c
; Sequence 33426, Application US/10793479
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2, REG
; CURRENT APPLICATION NUMBER: US/10/793,479
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US/09/513,999
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 33426
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-793-479-33426

Query Match          19.8%; Score 19; DB 6; Length 170;
Best Local Similarity 52.9%; Pred. No. 5.7e+02;
Matches 27; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY      25  CUUACCGCGUAUGCUGCCTCCCAUCCGGAACGCUCUAUACCCAGAGG 75
DB      87  CTAGACGCTTAATCTCTCCACCCTATACCCCTACTCCCAGCAGACGG 37

RESULT 15
US-10-803-180-1484/c
; Sequence 1484, Application US/10803180
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THE
; FILE REFERENCE: CL001511
; CURRENT APPLICATION NUMBER: US/10/803,180
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1484
; LENGTH: 194
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-180-1484

Query Match          19.8%; Score 19; DB 6; Length 194;
Best Local Similarity 55.6%; Pred. No. 5.9e+02;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY      35  UUAUGCUGCUCUCCCAUUCGGAACGCUCUAUACCCAGAGGUGCA 79
DB      107  TAAAGGYTTAACCCCAATCCCAAGTGTGTAAGAAACCCAGAGGCTGA 63

```

```

;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43955877
US-10-785-782-8362

Query Match          19.8%; Score 19; DB 6; Length 51;
Best Local Similarity 60.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY      61  CUCAUAAACCAGAGGUCGAUAGUACUGGAGUCCGCC 95
DB      10  CTATAAACCTGAGGTCGAAAGCTCTGGATAGTC 44

RESULT 14
US-10-793-479-33426/c
; Sequence 33426, Application US/10793479
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2, REG
; CURRENT APPLICATION NUMBER: US/10/793,479
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US/09/513,999
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 33426
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-793-479-33426

Query Match          19.8%; Score 19; DB 6; Length 170;
Best Local Similarity 52.9%; Pred. No. 5.7e+02;
Matches 27; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

QY      25  CUUACCGCGUAUGCUGCCTCCCAUCCGGAACGCUCUAUACCCAGAGG 75
DB      87  CTAGACGAGCTTAATCTCCACCCTATACCCCTACTCCCAGCAGACGCG 37

RESULT 15
US-10-803-180-1484/c
; Sequence 1484, Application US/10803180
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THE
; FILE REFERENCE: CL001511
; CURRENT APPLICATION NUMBER: US/10/803,180
; CURRENT FILING DATE: 2004-03-18
; NUMBER OF SEQ ID NOS: 6676
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1484
; LENGTH: 194
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-803-180-1484

Query Match          19.8%; Score 19; DB 6; Length 194;
Best Local Similarity 55.6%; Pred. No. 5.9e+02;
Matches 25; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY      35  UUAUGCUGCUCUCCCAUUCGGAACGCUCUAUACCCAGAGGUGCA 79
DB      107  TAAAGGYTTAACCCCAATCCCAAGTGTGTAAGAAACCCAGAGGCTGA 63

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Search completed: April 9, 2004, 09:18:37
Job time : 308.071 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 02:50:24 ; Search time 2937.6 Seconds
(without alignments)
975.888 Million cell updates/sec

Title: US-09-963-827B-3

Perfect score: 96

Sequence: 1 gggagagaggaagggaug.....cgauagacuggaucacccc 96

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 3354136

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_ges_hum:*
18: em_ges_inv:*
19: em_ges_pln:*
20: em_ges_vrt:*
21: em_ges_fun:*
22: em_ges_mam:*
23: em_ges_mus:*
24: em_ges_pro:*
25: em_ges_rod:*
26: em_ges_pbg:*
27: em_ges_vrl:*
28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27.6	28.8	139	28	AZ304985
C 2	27.2	28.3	197	29	CE086809
C 3	25.8	26.9	199	12	BG148573
C 4	25.6	26.7	197	10	BE009953

5	25.4	26.5	175	10	BF000123
6	25.2	26.2	176	9	AA168469
C 7	24	25.0	159	9	AV081297
8	24	25.0	161	9	AV410806
C 9	23.8	24.8	200	29	CE002581
C 10	23.4	24.4	117	29	EX893710
11	23.4	24.4	167	28	AZ603534
12	23.4	24.4	174	28	AQ934191
C 13	23.4	24.4	181	9	AA414435
C 14	23.4	24.4	190	12	BI082921
C 15	23.2	24.2	167	10	BB398492
C 16	23.2	24.2	190	28	AQ545235
17	23.2	24.2	192	13	BY317529
18	23	24.0	155	14	CD150229
C 19	23	24.0	155	14	CD150280
C 20	23	24.0	179	28	AQ537838
21	23	24.0	187	12	BI013417
22	22.8	23.8	107	29	CG559758
C 23	22.8	23.8	166	13	BQ636379
C 24	22.8	23.8	187	9	AL035806
25	22.8	23.8	187	10	BF486945
26	22.8	23.8	190	9	AV173481
C 27	22.8	23.8	192	14	CF641378
C 28	22.8	23.8	193	14	CF060123
C 29	22.8	23.8	193	14	CF060356
C 30	22.8	23.8	197	14	CF081678
C 31	22.6	23.5	186	28	CG373112
C 32	22.6	23.5	189	9	AA737145
C 33	22.6	23.5	197	13	BY082301
C 34	22.6	23.5	199	9	AA860648
35	22.4	23.3	124	13	BQ976411
36	22.4	23.3	127	10	BF364058
37	22.4	23.3	128	10	BF533294
38	22.4	23.3	133	14	NG2783
39	22.4	23.3	144	10	AW797027
40	22.4	23.3	162	12	BI431277
C 41	22.4	23.3	163	13	EX098115
C 42	22.4	23.3	171	10	AW604870
C 43	22.4	23.3	173	9	AV068579
44	22.4	23.3	185	10	BB044946
45	22.4	23.3	186	29	CE443923

ALIGNMENTS

RESULT 1

AZ304985

LOCUS

DEFINITION

AZ304985 139 bp DNA linear GSS 29-SEP-2000
1M0005C08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0005C08 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 139)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

1 GGGAGAGGAAGAGGGGACUUAACGGCGUAUUGCGUCCCAUUCGGAACG 60
101 GGGGAGAGCATCAGCAAGAGGACCTTATAATGTGACTCTGCTCCAACCTTGATGCTG 42
61 CUCAUAACCCGAGGUGCAUUAUACUGGAUCC 93
41 TTATGTGTCGAGGTAGCTGTATGATATCCC 9

Homo sapiens (human)
Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1. (bases 1 to 197)
Dias, Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matukuma, A., Bata, G. S., Simpson, D. H.,
Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V.,
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

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Location/Qualifiers
1. 197
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0174"
/note="Organ: breast normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

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BF000123 175 bp mRNA linear EST 06-OCT-2000
7h18b01.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:3316297 3',
similar to TR:Q9W6S3 Q9W6S3 SAPK INTERACTING PROTEIN. 1, mRNA
sequence.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: MCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LUNL, send email to:
info@image.llnl.gov

Source

ORIGIN

30 CCGGUAUGCUGCUCUCCCCAUCCGGAAAGGCUCAAAACCCAGAGGUCGAU 80
||||| :||| ||| | :||| ||| :
92 CGGCCCTGTTCATGTTTCAATTTCGCTAATTAAGTGACGACTCATGACCTGTT 122

AA168469 176 bp mRNA linear EST 16-FEB-1997
mr29b03.r1 Soares mouse 3bMS Mus musculus cDNA clone IMAGE:598829
5', mRNA sequence.
AA168469
AA168469.1 GI:174690
EST.

KEYWORDS

Query Match	24.8%	Score 23.8;	DB 29;	Length 200;
Best Local Similarity	53.7%;	Pred. No. 3.6e+03;		
Matches 36; Conservative	4;	Mismatches 27;	Indels 0;	Caps 0;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 190)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11056 row: f column: 23
High quality sequence stop: 94.
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1. 190
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/db_xref="taxon:10090"
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/tissue_type="tumor, biopsy sample"
/dev_stages="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Salt;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 24.4%; Score 23.4; DB 12; Length 190;
Best Local Similarity 67.6%; Pred. No. 4.8e+03;
Matches 23; Conservative 4; Mismatches 7; Indels 0; Gaps 0

QY 4 AGAGAGGAAGGAGGGAUGGGACUAUACCGCGUAA 37
|||||
DB 117 AGAGAGGAAGGAGGATGTGTTCTACAGCGCTAA 84
|||||

RESULT 15
BB398492
LOCUS
DEFINITION

BB398492 167 bp mRNA linear EST 15-JUL-2000
BB398492 RIKEN full-length enriched, ES cells Mus musculus cDNA
clone C33000SG22 3', similar to AF087680 Mus musculus valyl-tRNA
synthetase (Gta) mRNA, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

BB398492
BB398492.1 GI:9217888
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 167)

REFERENCE
AUTHORS

Kanno H., Aizawa K., Akahira S., Akiyama J., Arakawa T.,
Carninci P., Endo T., Fukuda S., Fukunishi Y., Hara A., Hayatsu N.,
Hirozane T., Hori F., Ishii Y., Ishikawa J., Ishikawa T., Itoh M.,
Izawa M., Kadota K., Kagawa I., Kai C., Kawai J., Kikuchi N.,
Kiyosawa H., Kojima Y., Kondo S., Koya S., Kurihara C.,
Kusakabe M., Matsuyama T., Miki R., Mizuno Y., Nakamura M., Oda H.,
Okazaki Y., Ono T., Owa C., Saito H., Sakai C., Sato K.,
Shibata K., Shibata Y., Shigemoto Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suganara Y., Suzuki H., Suzuki H., Tagawa A.,
Takahashi F., Tomimaga N., Toya T., Tanoda Y., Watahiki A.,
Watanabe S., Yamamura T., Yamanaka I., Yano R., Yasunishi A.,
Yokota T., Yoshida K., Yoshiki A., Yoshino M., Muramatsu M. and
Hayashizaki Y.
RIKEN Mouse ESTs (Konno H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 01:42:24 ; Search time 283.067 Seconds
(without alignments)
5206.064 Million cell updates/sec

Title: US-09-963-827B-70
Perfect score: 34
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 2199298

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_htg.*
- 3: gb_in.*
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- 5: gb_ov.*
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- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ste.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
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- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
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- 34: em_htg_pln.*
- 35: em_htg_rtd.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.2	50.6	77	6	AX902260 Sequence
2	17.2	50.6	77	6	BD037793 Sequence
3	17.2	50.6	115	6	AR422268 Sequence
4	17.2	50.6	115	6	BD117821 Sequence
5	17.2	50.6	196	6	BD275880 COMPOUNDS
6	17.2	50.6	196	6	AR220665 Sequence
7	17.2	50.6	196	6	AR255659 Sequence
8	17.2	50.6	196	6	AR281229 Sequence
9	17.2	50.6	196	6	AX355924 Sequence
10	17	50.0	104	10	S42430 T cell rece
11	17	50.0	123	10	U26786 Mus musculu
12	17	50.0	135	10	AY089788 Mus muscu
13	17	50.0	157	10	AF012183 Mus muscu
14	17	50.0	176	11	AU048750 Rattus no
15	17	50.0	186	8	PCH543747 Phaneroch
16	16.8	49.4	188	11	H0MSWX854 Human chrom
17	16.2	47.6	161	1	AY040741 Unculture
18	16	47.1	85	9	HUMLP31 Homo sapien
19	16	47.1	113	5	AMTMA2A Ambystoma m
20	16	47.1	127	4	AF006569 Sus scrof
21	16	47.1	189	1	CLJ536093 Unculture
22	15.8	46.5	94	9	F193462S03 Pan trogl
23	15.8	46.5	160	1	AY013620 Unculture
24	15.8	46.5	167	1	AF509475 Bacterium
25	15.8	46.5	180	9	HAI9270 Homo sapi
26	15.6	45.9	141	6	AX913011 Sequence
27	15.6	45.9	141	6	BD048544 Sequence
28	15.6	45.9	159	9	F193462S14 Pan trogl
29	15.4	45.3	38	6	AR286969 Sequence
30	15.4	45.3	38	6	AX398959 Sequence
31	15.4	45.3	64	6	AX202684 Sequence
32	15.4	45.3	78	10	AF096388 Mus muscu
33	15.4	45.3	78	10	AF096389 Mus muscu
34	15.4	45.3	87	10	AF096378 Mus muscu
35	15.4	45.3	123	10	AY089787 Mus muscu
36	15.4	45.3	147	6	ARI73337 Sequence
37	15.4	45.3	151	10	HAMADBL1 Adenovirus
38	15.4	45.3	160	9	HSU32641 Human ret/P
39	15.4	45.3	163	1	AF528054 Haemophil
40	15.4	45.3	164	10	MMARK001 X56257 Mouse monon
41	15.4	45.3	183	11	HUMUT452A L29983 Human STS U
42	15.4	45.3	190	1	ASP493433 Agrobacte
43	15.4	45.3	190	1	NSP493434 Neisseria
44	15.4	45.3	196	9	HS170810R Z57295 H.sapiens C
45	15.4	45.3	198	11	G26726 human STS S

ALIGNMENTS

RESULT 1	AX902260	Sequence 18123 from Patent EP1033401.	77 bp	DNA	linear	PAT 18-DEC-2003
LOCUS	AX902260	Sequence 18123 from Patent EP1033401.				
DEFINITION	AX902260					
ACCESSION	AX902260					
VERSION	AX902260.1	GI:40057217				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.					
TITLE	Expressed sequence tags and encoded human proteins					
JOURNAL	Patent: EP 1033401-A 18123 06-SEP-2000;					

2

```

Unclassified.
REFERENCE 1 (bases 1 to 196)
AUTHORS Wang,T., Hosken,N.A., Kalos,M.D., Fanger,G.R. and Fan,L.
TITLE Compounds and methods for therapy and diagnosis of lung cancer
JOURNAL Patent: US 6482597-A 317 19-NOV-2002;
FEATURES Location/Qualifiers
source 1..196
/mol_type="genomic DNA"

ORIGIN
Query Match 50.6%; Score 17.2; DB 6; Length 196;
Best Local Similarity 55.7%; Pred. No. 8.2e+04;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0

Qy 3 GGGGACUAUACCGGUAUUGCGUCGCCCC 32
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Db 104 GGAGATTGGACGGCGCTGATGCTCCCTCCC 133

RESULT 8
AR281229 LOCUS 196 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 317 from patent US 6518256.
ACCESSION AR281229
VERSION AR281229.1 GI:29716706
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 196)
AUTHORS wang,T., Fan,L., Kalos,M.D., Bangur,C.S., Hosken,N.A. and
Fanger,G.R.
TITLE Compounds and methods for therapy and diagnosis of lung cancer
JOURNAL Patent: US 6518256-A 317 11-FEB-2003;
FEATURES Location/Qualifiers
source 1..196
/mol_type="genomic DNA"

ORIGIN
Query Match 50.6%; Score 17.2; DB 6; Length 196;
Best Local Similarity 55.7%; Pred. No. 8.2e+04;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 3 GGGGACUAUACCGGUAUUGCGUCGCCCC 32
||| : : : : : : : : : : : : : : : : :
Db 104 GGAGATTGGACGGCGCTGATGCTCCCTCCC 133

RESULT 9
AX365924 LOCUS 196 bp DNA linear PAT 15-FEB-2003
DEFINITION Sequence 317 from Patent WO0200174.
ACCESSION AX365924
VERSION AX365924.1 GI:18697433
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A.,
Mcneil,P.D., Fanger,N., Retter,M.W., Marnierakis,M., Fanger,G.R.,
Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W.
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 0200174-A 317 03-JAN-2002;
JOURNAL CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
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ORIGIN
Query Match          50.6%; Score 17.2; DB 6; Length 196;
Best Local Similarity 56.7%; Pred. No. 8.2e+04;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAACCGCUAUGCUCUCCCC 32
DB 104 GGAGATTGGACGGCGTGATGCTCCCTCCCC 133

RESULT 10
S42430 LOCUS          104 bp      DNA      linear      ROD 08-MAY-1993
DEFINITION          T cell receptor alpha chain, T cell receptor alpha chain
                    {nonproductive rearrangement} [mice, HLA-Cw3-reactive CTL clone
                    Cw3/1.1, Genomic, 104 nt].
ACCESSION          S42430
VERSION            S42430.1 GI:253590
KEYWORDS
SOURCE            Mus sp.
ORGANISM          Mus musculus (house mouse)
REFERENCE
AUTHORS            Shih,F.F., Cerasoli,D.M. and Caton,A.J.
TITLE              A major T cell determinant from the influenza virus hemagglutinin
                    (HA) can be a cryptic self peptide in HA transgenic mice
JOURNAL            Int. Immunol. 9 (2), 249-261 (1997)
MEDLINE            97192188
PUBMED             9040007
REFERENCE          2 (bases 1 to 123)
AUTHORS            Shih,F.F.
TITLE              Direct Submission
JOURNAL            Submitted (09-MAY-1995) Pei F. Shih, The Wistar Institute of
                    Anatomy and Chemistry, 3601 Spruce Street, Philadelphia, PA 19104,
                    USA
FEATURES
source            Location/Qualifiers
                    1..123
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                    /mol_type="mRNA"
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CDS
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                    /note="This sequence comes from Fig. 3B"

gene
CDS
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Best Local Similarity 60.0%; Pred. No. 1.2e+05;
Matches 15; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 UGGGACUUAACCGCUAUGCUC 26
DB 6 TGGGGACTCAGCCGCTCTCTGC 30

RESULT 12
AY089788 LOCUS          135 bp      mRNA      linear      ROD 01-OCT-2002
DEFINITION          Mus musculus TRP-2 specific T-cell receptor AV5 mRNA, partial cds.
ACCESSION          AY089788
VERSION            AY089788.1 GI:23428649
KEYWORDS
SOURCE            Mus musculus (house mouse)
ORGANISM          Mus musculus
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS            De Palma,R., Del Galdo,F., Milan,G. and Bronte,V.
TITLE              Analysis of T cell receptor repertoire of CTL recognizing the mouse
                    melanocyte differentiation antigen TRP-2
JOURNAL            Unpublished
AUTHORS            2 (bases 1 to 135)
TITLE              De Palma,R., Del Galdo,F., Milan,G. and Bronte,V.
JOURNAL            Submitted (13-MAR-2002) Clinical and Experimental Medicine, II
                    University of Naples, S. Pansini 5, Naples 80131, Italy
FEATURES
source            Location/Qualifiers
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/organism="Mus musculus"
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ORIGIN
Query Match          50.0%; Score 17; DB 10; Length 135;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 15; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 UGGGGACUUAACCGCGUAUAGCUGC 26
    :||||: |||||: |||||: |||||:
Db 9 TGGGGACTCAGCGCGTACTTCTGC 33

RESULT 13
AF012183
LOCUS          Mus musculus T-cell receptor alpha chain (TCRA) mRNA, partial cds.
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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<!.>97
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103..152
/gene="TCRA"
/notes="J_region 35"

CDS
gene
CDS
V_region
J_segment
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C_region          153..157
ORIGIN
Query Match          50.0%; Score 17; DB 10; Length 157;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 15; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 UGGGGACUUAACCGCGUAUAGCUGC 26
    :||||: |||||: |||||: |||||:
Db 66 TGGGGACTCAGCGCGTACTTCTGC 90

RESULT 14
AU048750
LOCUS          Rattus norvegicus, OTSUKA clone, 765bp DNA linear STS 20-JAN-2000
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/mol_type="genomic DNA"
/strain="Brown Norway"
/db_xref="taxon:10116"
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765allR=5'-TCGATCAATCCAGGCAAA-3'"

ORIGIN
Query Match          50.0%; Score 17; DB 11; Length 176;
Best Local Similarity 60.0%; Pred. No. 1e+05;
Matches 15; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 5 GGACUUAACCGCGUAUAGCUGCUC 29
    |||:||||: |||||: |||||: |||||:
Db 36 GGGCTATACAGAGAAATGTCCTC 60

RESULT 15
PCH543747
LOCUS          Phanerochaete chrysosporium partial mRNA for putative Hsp70 protein
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
Source
186bp mRNA linear PJN 12-FEB-2003
Phanerochaete chrysosporium partial mRNA for putative Hsp70 protein
(hsp70 gene).
AJ543747
AJ543747.1 GI:28372047
hsp70 gene; Hsp70 protein.
Phanerochaete chrysosporium (anamorph: Sporotrichum pruinosum)
Phanerochaete chrysosporium
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
```

Aphyllophorales; Corticiaceae; Phanerochaete.

REFERENCE 1
AUTHORS Asmann, E.M.
TITLE Iron-responsive genes in Phanerochaete chrysosporium
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 186)
AUTHORS Asmann, E.M.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2003) Asmann E.M., Cmeg, Universidade Estadual de Campinas, Caixa Postal 6010, Campinas, Sao Paulo, 13093-020, BRAZIL

FEATURES
source Location/Qualifiers
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/db_xref="taxon:5306"
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/gene="hsp70"
/codon_start=1
/product="putative Hsp70 protein"
/protein_id="CAD66422.1"
/db_xref="GI:28372048"
/translation="ALLIVPPSHRQXCCHRMQGQVLIIDAGGGTVDLSSYCFISLSPI
AVEETAPXNERGAYLLEL"

ORIGIN

Query Match 50.0%; Score 17; DB 8; Length 186;
Best Local Similarity 48.5%; Pred. No. 1e+05;
Matches 16; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 UGGGACUUAACCGGUAAUGCGUCCUCCCAU 34
:|||||:|||||:|||||:|||||:
DB 90 TGTGACTTGAGCTGCTGCTTCTCTCTT 122

Search completed: April 9, 2004, 03:53:27
Job time : 286.067 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 01:39:24 ; Search time 120.8 Seconds
(without alignments)
1195.685 Million cell updates/sec

Title: US-09-963-827B-70

Perfect score: 34

Sequence: 1 auggggacuaacccgcuauagcuccccau 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124098041 residues

Total number of hits satisfying chosen parameters: 3774412

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	34	6	ABN88557
2	34	100.0	35	7	ABZ21241
3	34	100.0	38	7	ABZ21259
4	34	100.0	40	7	ABZ21242
5	34	100.0	96	6	ABN88490
6	21	61.8	23	7	ABZ21269
7	17.2	50.6	77	3	AAI14048
8	17.2	50.6	100	7	ACD79614
9	17.2	50.6	196	3	AAI66013
10	17.2	50.6	196	6	ABL49232
11	17.2	50.6	196	6	ABQ92418
12	17.2	50.6	196	8	ADA28407
13	17	50.0	17	7	ABZ21265
14	17	50.0	17	7	ABZ21277
15	17	50.0	18	7	ABZ21266
16	17	50.0	20	7	ABZ21260
17	17	50.0	46	2	AAI43544
18	17	50.0	112	4	AAI24741
19	17	50.0	112	4	ABA70029
20	17	50.0	112	4	AAI50142
21	17	50.0	112	4	ABA36840
22	17	50.0	112	4	AAK44134
23	17	50.0	112	4	AAK18238

C	24	17	50.0	112	4	ABS43790	Human liv
C	25	17	50.0	112	6	ABS18369	Human gen
C	26	16.2	47.6	113	4	ABA69564	Human foe
C	27	16.2	47.6	113	4	AAK43625	Human bon
C	28	16.2	47.6	113	4	AAK17785	Human bra
C	29	16.2	47.6	148	4	AAK67210	Human imm
C	30	15.8	46.5	51	4	AAI31035	Human SNP
C	31	15.6	45.9	31	7	ABZ21244	FIXa apta
C	32	15.6	45.9	33	7	ABZ21258	Aptamer 9
C	33	15.6	45.9	76	4	AAI48228	Enterococ
C	34	15.6	45.9	76	7	ACA12905	Prokaryot
C	35	15.6	45.9	141	3	ACA24799	Human sec
C	36	15.6	45.9	144	6	ABQ90618	M. capsul
C	37	15.6	45.9	164	4	AAI21015	Probe #10
C	38	15.6	45.9	164	4	ABA66087	Human foe
C	39	15.6	45.9	164	4	AAI46268	Probe #14
C	40	15.6	45.9	164	4	ABA48207	Human bra
C	41	15.6	45.9	164	4	ABA33163	Probe #11
C	42	15.6	45.9	164	4	AAK40252	Human bon
C	43	15.6	45.9	164	4	AAK14510	Human bra
C	44	15.6	45.9	164	4	ABS39826	Human liv
C	45	15.6	45.9	164	5	AAI06732	Probe #67

ALIGNMENTS

RESULT 1

ABN88557
ID ABN88557 standard; RNA; 34 BP.

AC ABN88557;

DT 19-AUG-2002 (first entry)

XX Coagulation factor IXa (FIXa) aptamer SEQ ID NO:70.

DE RNA aptamer; identification; coagulation factor; angiotensin; thrombin;
KW E2F family; cardiant; cytosolic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.

XX Homo sapiens.

OS Synthetic.

XX WO200226932-A2.

XX 04-APR-2002.

XX 26-SEP-2001; 2001WO-US030004.

XX 26-SEP-2000; 2000US-0235654P.

XX (UYDU-) UNIV DUKE.

XX Sullenger BA, Rusconi CP;

XX WPI; 2002-479560/51.

XX Novel RNA aptamers that selectively bind coagulation pathway factors, E2F family members, Ang1 or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.

XX Claim 14; Page 25; 216pp; English.

XX The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiotensin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have cardiant and cytosolic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that

CC the biological activity of the coagulation pathway factor in the warm-
 CC blooded vertebrate is modulated. (I) are also useful for treating
 CC cardiovascular diseases in the mammal. (II) are useful for modulating B2F
 CC activity in a warm-blooded vertebrate. (III) are useful for modulating
 CC Angi or Ang2 activity in a warm-blooded vertebrate. (I) are potent
 CC anticoagulants and significantly delay the clotting time of normal human
 CC plasma or the activation of platelets in response to thrombin. (II) are
 CC useful for inhibiting cell proliferation in a number of conditions e.g.,
 CC intimal hyperplasia following bypass graft surgery. (III) are useful for
 CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
 CC research and therapeutic context. The aptamers are useful as diagnostic
 CC reagents to detect the presence or absence of target substances to which
 CC they specifically bind, and for identifying substances to which they
 CC specifically bind, for isolating and purifying substances to which they
 CC bind, and as a separation reagent for retrieving the targets to which
 CC they specifically bind. ABN8488 to ABN89713 and ABB81231 represent
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 34 BP; 7 A; 11 C; 8 G; 0 T; 8 U; 0 Other;

Query Match 100.0%; Score 34; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AUGGGGACUUAACCGGUAAUGCGUCCUCCCAU 34
 |||||
 Db 1 AUGGGGACUUAACCGGUAAUGCGUCCUCCCAU 34

RESULT 2
 ABZ21241
 ID ABZ21241 standard; RNA; 35 BP.
 XX
 AC ABZ21241;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE FIXA aptamer, 9.3t, SEQ ID 1.
 XX
 KW Immunosuppressive; aptamer; infection; autoimmunity; tumour;
 KW inflammatory proliferative disease; hypoglycaemia; human;
 KW coagulation Factor IXa; FIXa; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..35
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "All purines are 2'-hydroxyl and pyrimidines are 2'
 FT -fluoro nucleotides"
 FT misc_binding 1..7
 FT /tag= b
 FT /bound_moiety= "Nucleotides 28..34"
 FT stem_loop 15..26
 FT /tag= c
 FT misc_binding 28..34
 FT /tag= d
 FT /bound_moiety= "Nucleotides 1..7"
 FT modified_base 35
 FT /tag= e
 FT /mod_base= OTHER
 FT /note= "idt"
 XX
 PN WO200296926-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 28-MAY-2002; 2002WO-US016555.
 XX
 PR 25-MAY-2001; 2001US-0293231P.
 PR 07-NOV-2001; 2001US-0331037P.
 XX

PA (UYDU-) UNIV DUKE.
 XX Sullenger BA, Rusconi C;
 XX WPI; 2003-140438/13.
 XX
 PT Altering affinity of nucleic acid ligands for target molecules in a
 PT patient or reversing binding of labeled ligands to target tissues, by
 PT administering (to a patient receiving the ligand) a modulator that binds
 PT to ligand.
 XX
 PS Example 1; Fig 1; 111pp; English.
 XX
 CC The present invention relates to a method for altering the affinity of a
 CC nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
 CC or in vitro, or reversing the binding of the labelled ligand to a target
 CC tissue. The method comprises administering a modulator that binds to the
 CC ligand to a patient receiving the ligand, or contacting the ligand with
 CC the modulator under conditions such that the modulator binds to the
 CC ligand, and thus alters the affinity of the ligand for the target
 CC molecule. The method is useful for treating a number of disorders e.g.
 CC infection, autoimmunity, tumours, inflammatory proliferative diseases and
 CC hypoglycaemia. The present sequence is a nuclease-resistant 2'-fluoro
 CC pyrimidine-modified aptamer to human coagulation Factor IXa (FIXa
 CC aptamer), which was used to illustrate the method of the invention
 XX
 SQ Sequence 35 BP; 7 A; 11 C; 8 G; 1 T; 8 U; 0 Other;
 Query Match 100.0%; Score 34; DB 7; Length 35;
 Best Local Similarity 100.0%; Pred. No. 6.8e-06;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AUGGGGACUUAACCGGUAAUGCGUCCUCCCAU 34
 |||||
 Db 1 AUGGGGACUUAACCGGUAAUGCGUCCUCCCAU 34
 RESULT 3
 ABZ21259
 ID ABZ21259 standard; RNA; 38 BP.
 XX
 AC ABZ21259;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Tailed aptamer 9.3t-3NT, SEQ ID 19.
 XX
 KW Immunosuppressive; aptamer; infection; autoimmunity; tumour;
 KW inflammatory proliferative disease; hypoglycaemia; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
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 FT /tag= a
 FT /bound_moiety= "Nucleotides 28..34"
 FT stem_loop 15..26
 FT /tag= b
 FT misc_binding 28..34
 FT /tag= c
 FT /bound_moiety= "Nucleotides 1..7"
 FT modified_base 35..38
 FT /tag= e
 FT /mod_base= OTHER
 FT /note= "mG mU mC idT"
 XX
 PN WO200296926-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 28-MAY-2002; 2002WO-US016555.
 XX
 PR 25-MAY-2001; 2001US-0293231P.
 PR

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PR 07-NOV-2001; 2001US-0331037P.
XX (UYDU-) UNIV DUKE.
XX Sullenger BA, Rusconi C;
XX WPI; 2003-140438/13.
XX
XX Altering affinity of nucleic acid ligands for target molecules in a
XX patient or reversing binding of labeled ligands to target tissues, by
XX administering (to a patient receiving the ligand) a modulator that binds
XX to ligand.
XX
XX Example 4; Fig 11; ilpp; English.
XX
XX The present invention relates to a method for altering the affinity of a
XX nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
XX or in vitro, or reversing the binding of the labelled ligand to a target
XX tissue. The method comprises administering a modulator that binds to the
XX ligand to a patient receiving the ligand, or contacting the ligand with
XX the modulator under conditions such that the modulator binds to the
XX ligand, and thus alters the affinity of the ligand for the target
XX molecule. The method is useful for treating a number of disorders e.g.
XX infection, autoimmunity, tumours, inflammatory proliferative diseases and
XX hypoglycaemia. The present sequence is an aptamer which was used to
XX illustrate the method of the invention
XX
XX Sequence 38 BP; 7 A; 12 C; 9 G; 1 T; 9 U; 0 Other;
XX
XX Query Match 100.0%; Score 34; DB 7; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 6.9e-06;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AUGGGGACUUAUACCGGUAUUGCGUAGUCGUCUCCCAU 34
XX |||||
XX Db 1 AUGGGGACUUAUACCGGUAUUGCGUAGUCGUCUCCCAU 34
XX |||||

RESULT 4
ABZ21242
ID ABZ21242 standard; RNA; 40 BP.
XX
XX AC ABZ21242;
XX
XX 16-APR-2003 (first entry)
XX
XX DE FIXa aptamer, SEQ ID 2.
XX
XX Immunosuppressive; aptamer; infection; autoimmunity; tumour;
XX inflammatory proliferative disease; hypoglycaemia; human;
XX coagulation Factor IXa; FIXa; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
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XX /bound_moiety= "Nucleotides 31..40"
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XX stem_loop 16..25
XX /*tag= b
XX misc_binding 31..40
XX /*tag= c
XX /bound_moiety= "Nucleotides 1..10"
XX
XX WO200296926-A1.
XX
XX 05-DEC-2002.
XX
XX 28-MAY-2002; 2002WO-US016555.
XX
XX 25-MAY-2001; 2001US-0293231P.
XX 07-NOV-2001; 2001US-0331037P.
XX

```

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PA (UYDU-) UNIV DUKE.
XX Sullenger BA, Rusconi C;
XX WPI; 2003-140438/13.
XX
XX Altering affinity of nucleic acid ligands for target molecules in a
XX patient or reversing binding of labeled ligands to target tissues, by
XX administering (to a patient receiving the ligand) a modulator that binds
XX to ligand.
XX
XX Example 2; Fig 7; ilpp; English.
XX
XX The present invention relates to a method for altering the affinity of a
XX nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
XX or in vitro, or reversing the binding of the labelled ligand to a target
XX tissue. The method comprises administering a modulator that binds to the
XX ligand to a patient receiving the ligand, or contacting the ligand with
XX the modulator under conditions such that the modulator binds to the
XX ligand, and thus alters the affinity of the ligand for the target
XX molecule. The method is useful for treating a number of disorders e.g.
XX infection, autoimmunity, tumours, inflammatory proliferative diseases and
XX hypoglycaemia. The present sequence is an aptamer to human coagulation
XX Factor IXa (FIXa aptamer), which was used to illustrate the method of the
XX invention
XX
XX Sequence 40 BP; 7 A; 13 C; 11 G; 0 T; 9 U; 0 Other;
XX
XX Query Match 100.0%; Score 34; DB 7; Length 40;
XX Best Local Similarity 100.0%; Pred. No. 6.9e-06;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AUGGGGACUUAUACCGGUAUUGCGUAGUCGUCUCCCAU 34
XX |||||
XX Db 4 AUGGGGACUUAUACCGGUAUUGCGUAGUCGUCUCCCAU 37
XX |||||

RESULT 5
ABN88490
ID ABN88490 standard; RNA; 96 BP.
XX
XX AC ABN88490;
XX
XX 19-AUG-2002 (first entry)
XX
XX DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:3.
XX
XX RNA aptamer; identification; coagulation factor; angiotensin; thrombin;
XX E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
XX cell proliferation; intimal hyperplasia; angiogenesis;
XX bypass graft surgery; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200226932-A2.
XX
XX 04-APR-2002.
XX
XX 26-SEP-2001; 2001WO-US030004.
XX
XX 26-SEP-2000; 2000US-0235654P.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Sullenger BA, Rusconi CP;
XX WPI; 2002-479560/51.
XX
XX Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
XX family members, Angi or Ang2, useful for modulating coagulation pathway
XX factor activity, E2F activity and Angi or Ang2 activity in a mammal.
XX

```

PS Claim 13; Fig 1A; 216pp; English.

XX The present invention describes RNA aptamers (I,II,III) that selectively

CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)

CC angiotensin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have

CC a dissociation constant for the coagulation pathway factor, an E2F family

CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have

CC cardiac and cytostatic activities. (I) are useful for modulating the

CC biological activity of a coagulation pathway factor which involves

CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that

CC the biological activity of the coagulation pathway factor in the warm-

CC blooded vertebrate is modulated. (I) are also useful for treating

CC cardiovascular diseases in the mammal. (II) are useful for modulating

CC activity in a warm-blooded vertebrate. (III) are useful for modulating

CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent

CC anticoagulants and significantly delay the clotting time of normal human

CC plasma or the activation of platelets in response to thrombin. (II) are

CC useful for inhibiting cell proliferation in a number of conditions e.g.,

CC intimal hyperplasia following bypass graft surgery. (III) are useful for

CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,

CC research and therapeutic context. The aptamers are useful as diagnostic,

CC reagents to detect the presence or absence of target substances to which

CC they specifically bind, and for identifying substances to which they

CC specifically bind, for isolating and purifying substances to which they

CC bind, and as a separation reagent for retrieving the targets to which

CC they specifically bind. ABR88488 to ABR88713 and ABR81231 represent

CC sequences used in the exemplification of the present invention

XX

SQ Sequence 96 BP; 24 A; 27 C; 29 G; 0 T; 16 U; 0 Other;

Query Match 100.0%; Score 34; DB 6; Length 96;

Best Local Similarity 100.0%; Pred. No. 8.1e-06;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUGGGGACUUAACCGGUAAUGCCUCCUCCCAU 34

Db ||||||||||||||||||||||||||||||||||

18 AUGGGGACUUAACCGGUAAUGCCUCCUCCCAU 51

RESULT 6

ID ABZ21269/c

AC ABZ21269

AC ABZ21269;

DT 16-APR-2003 (first entry)

XX

DE Fixa aptamer 9.3t&9.3t-3NT oligonucleotide modulator, AS 5-1, SEQ ID 29.

XX

KW Immunosuppressive; aptamer; infection; autoimmunity; tumour;

KW inflammatory proliferative disease; hypoglycaemia; human;

KW coagulation Factor Ixa; Fixa; ss.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT modified_base 1..23

FT /*tag= a

FT /mod_base= OTHER

FT /note= "All nucleotides are 2'Omethyl oligonucleotides"

XX

PN WO200296926-A1.

XX

PD 05-DEC-2002.

XX

PF 28-MAY-2002; 2002WO-US016555.

XX

PR 25-MAY-2001; 2001US-0293231P.

PR 07-NOV-2001; 2001US-0331037P.

XX

PA (UYDU-) UNIV DUKE.

XX

PI Sullenger BA, Rusconi C;

XX

XX WPI; 2003-140438/13.

XX Altering affinity of nucleic acid ligands for target molecules in a

PT patient or reversing binding of labeled ligands to target tissues, by

PT administering (to a patient receiving the ligand) a modulator that binds

PT to ligand.

XX

PS Claim 50; Page 74; 11pp; English.

XX

CC The present invention relates to a method for altering the affinity of a

CC nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient

CC or in vitro, or reversing the binding of the labelled ligand to a target

CC tissue. The method comprises administering a modulator that binds to the

CC ligand to a patient receiving the ligand, or contacting the ligand with

CC the modulator under conditions such that the modulator binds to the

CC ligand, and thus alters the affinity of the ligand for the target

CC molecule. The method is useful for treating a number of disorders e.g.

CC infection, autoimmunity, tumours, inflammatory proliferative diseases and

CC hypoglycaemia. The present sequence is an oligonucleotide modulator, which

CC targets the FIXa aptamers 9.3t and 9.3t-3NT. The FIXa aptamers bind

CC to human coagulation Factor Ixa and were used to illustrate the method of

CC the invention. This oligonucleotide was found to be effective at

CC reversing FIXa aptamer's anticoagulation activity in human plasma in

CC vitro

XX

SQ Sequence 23 BP; 5 A; 7 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 61.8%; Score 21; DB 7; Length 23;

Best Local Similarity 81.0%; Pred. No. 6.4;

Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGGACUUAACCGGUAAUGC 23

Db ||||||:|||||:|||||

21 GGGGACTATACCGGTAATGC 1

RESULT 7

AC AAC14048

AC AAC14048;

XX

DT 06-OCT-2000 (first entry)

XX

DE Human secreted protein 5' EST, SEQ ID NO: 18123.

XX

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KW gene therapy; chromosome mapping; ss.

XX

OS Homo sapiens.

XX

PN EP1033401-A2.

XX

PD 06-SEP-2000.

XX

PF 21-FEB-2000; 2000EP-00200610.

XX

PR 26-FEB-1999; 99US-0122487P.

XX

PA (GEST) GENSET.

XX

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX

XX WPI; 2000-500381/45.

XX

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX

PS Claim 1; SEQ ID NO 18123; 71pp + Sequence Listing; English.

XX

CC The present sequence is one of a large number of 5' ESTs derived from


```
Best Local Similarity 56.7%; Pred. No. 5.4e+02;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAACCGGUAUAGCGGCUCCGCC 32
DB 104 GGAGATTGGACGGCCTGATGCTCCTCC 133

RESULT 10
ABL49232
ID ABL49232 standard; cDNA; 196 BP.
AC ABL49232;
XX
DT 01-MAY-2002 (first entry)
DE Human lung tumour cDNA sequence clone 25331 SEQ ID NO:317.
XX
KW Human; lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
KW immune response; ss.
XX
OS Homo sapiens.
XX
PN WO200200174-A2.
XX
PD 03-JAN-2002.
XX
PF 28-JUN-2001; 2001WO-US021055.
XX
PR 28-JUN-2000; 2000US-00606421.
PR 02-AUG-2000; 2000US-00630940.
PR 21-AUG-2000; 2000US-00643597.
PR 15-SEP-2000; 2000US-00662786.
PR 09-OCT-2000; 2000US-00685696.
PR 12-DEC-2000; 2000US-00735705.
PR 07-MAY-2001; 2001US-00850716.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Warnerakis M, Fanger GR;
PI Vedvick TS, Carter D, Watanabe Y, Peckham DW;
XX
DR WPI; 2002-090513/12.
XX
PT Polynucleotides encoding lung tumor polypeptides, useful for treating
PT lung cancer or stimulating an immune response.
XX
PS Example 1; Page 309-310; 374pp; English.
XX
CC The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies, fusion
CC proteins, T cell populations, or antigen presenting cells that express
CC the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABL74946 to
CC ABL75070 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 196 BP; 29 A; 52 C; 62 G; 53 T; 0 U; 0 Other;
Query Match 50.6%; Score 17.2; DB 6; Length 196;
Best Local Similarity 56.7%; Pred. No. 5.4e+02;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAACCGGUAUAGCGGCUCCGCC 32
DB 104 GGAGATTGGACGGCCTGATGCTCCTCC 133

RESULT 11
ABQ92418
ID ABL49232 standard; cDNA; 196 BP.
AC ABL49232;
XX
DT 07-OCT-2002 (first entry)
DE Human lung cancer associated cDNA sequence SEQ ID NO:317.
XX
KW Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine; gene;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200247534-A2.
XX
PD 20-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US047576.
XX
PR 12-DEC-2000; 2000US-00735705.
PR 07-MAY-2001; 2001US-00850716.
PR 28-JUN-2001; 2001US-00897778.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
PI McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
PI Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
XX
DR WPI; 2002-583465/62.
XX
PT Novel lung carcinoma polynucleotide sequences and polypeptides encoded by
PT the polynucleotides, useful in pharmaceutical compositions such as
PT vaccines and as markers to indicate the presence of lung cancer.
XX
PS Example 1; Page 317; 381pp; English.
XX
CC The present invention describes isolated human lung carcinoma
CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
CC activity, and can be used in gene therapy and in vaccines. Compositions
CC comprising (I) or (II) can be used for stimulating an immune response in
CC a patient and for treating lung cancer in a patient. Oligonucleotides of
CC (I) can be used for detecting the presence of a cancer in a patient, by
CC obtaining a biological sample from the patient, contacting the biological
CC sample with the oligonucleotide, detecting in the sample, an amount of
CC polynucleotide that hybridises to the oligonucleotide and comparing the
CC amount of polynucleotide that hybridises to the oligonucleotide to a
CC predetermined cut-off value, and determining the presence of a cancer in
CC the patient. (I) and (II) are useful in pharmaceutical compositions, e.g.
CC vaccines. (I) is useful as a marker to indicate the presence or absence
CC of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to
CC ABP61992 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 196 BP; 29 A; 52 C; 62 G; 53 T; 0 U; 0 Other;
Query Match 50.6%; Score 17.2; DB 6; Length 196;
Best Local Similarity 56.7%; Pred. No. 5.4e+02;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAACCGGUAUAGCGGCUCCGCC 32
DB 104 GGAGATTGGACGGCCTGATGCTCCTCC 133

RESULT 12
ADA28407
ID ADA28407 standard; cDNA; 196 BP.
XX
AC ADA28407;
XX
DT 20-NOV-2003 (first entry)
XX
```


RESULT 13
ABZ21265/C
ID ABZ212

```
DE FIXa aptamer oligonucleotide modulator, 5-2C, SEQ ID 41.
XX Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW inflammatory proliferative disease; hypoglycaemia; human;
XX coagulation Factor IXa; FIXa; ss.
OS Unidentified.
XX WO200296926-A1.
XX PD 05-DEC-2002.
XX PF 28-MAY-2002; 2002WO-US016555.
XX PR 25-MAY-2001; 2001US-0293231P.
XX PR 07-NOV-2001; 2001US-0331037P.
XX PA (UYDU-) UNIV DUKE.
XX PI Sullenger BA, Rusconi C;
XX DR WPI; 2003-140438/13.
XX DR WPI; 2003-140438/13.
XX PT Altering affinity of nucleic acid ligands for target molecules in a
PT patient or reversing binding of labeled ligands to target tissues, by
PT administering (to a patient receiving the ligand) a modulator that binds
PT to ligand.
XX Claim 50; Page 75; 11lpp; English.
XX CC The present invention relates to a method for altering the affinity of a
CC nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC or in vitro, or reversing the binding of the labelled ligand to a target
CC tissue. The method comprises administering a modulator that binds to the
CC ligand to a patient receiving the ligand, or contacting the ligand with
CC the modulator under conditions such that the modulator binds to the
CC ligand, and thus alters the affinity of the ligand for the target
CC molecule. The method is useful for treating a number of disorders e.g.
CC infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC hypoglycaemia. The present sequence is an oligonucleotide modulator,
CC which targets the FIXa aptamer 9.3t and 9.3t-3NT. The FIXa aptamers bind
CC to human coagulation Factor IXa and were used to illustrate the method of
CC the invention. This oligonucleotide was found to be effective at
CC reversing FIXa aptamer's anticoagulation activity in human plasma in
CC vitro
XX SQ Sequence 17 BP; 3 A; 6 C; 4 G; 0 T; 4 U; 0 Other;
Query Match 50.0%; Score 17; DB 7; Length 17;
Best Local Similarity 82.4%; Pred. No. 4.3e+02;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 AUGGGGACUUAACCGG 17
Db :|||||:|||||
17 ATGGGGACTATACCGG 1
RESULT 15
ABZ21266/c
ID ABZ21266 standard; RNA; 18 BP.
XX AC ABZ21266;
XX DT 16-APR-2003 (first entry)
XX DE FIXa aptamer 9.3t oligonucleotide modulator, Anti D T1, SEQ ID 26.
XX Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW inflammatory proliferative disease; hypoglycaemia; human;
XX coagulation Factor IXa; FIXa; ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT modified_base 1..18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "All nucleotides are 2'Omethyl oligonucleotides"
XX WO200296926-A1.
XX PD 05-DEC-2002.
XX PF 28-MAY-2002; 2002WO-US016555.
XX PR 25-MAY-2001; 2001US-0293231P.
XX PR 07-NOV-2001; 2001US-0331037P.
XX PA (UYDU-) UNIV DUKE.
XX PI Sullenger BA, Rusconi C;
XX DR WPI; 2003-140438/13.
XX DR WPI; 2003-140438/13.
XX PT Altering affinity of nucleic acid ligands for target molecules in a
PT patient or reversing binding of labeled ligands to target tissues, by
PT administering (to a patient receiving the ligand) a modulator that binds
PT to ligand.
XX Claim 50; Page 74; 11lpp; English.
XX CC The present invention relates to a method for altering the affinity of a
CC nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC or in vitro, or reversing the binding of the labelled ligand to a target
CC tissue. The method comprises administering a modulator that binds to the
CC ligand to a patient receiving the ligand, or contacting the ligand with
CC the modulator under conditions such that the modulator binds to the
CC ligand, and thus alters the affinity of the ligand for the target
CC molecule. The method is useful for treating a number of disorders e.g.
CC infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC hypoglycaemia. The present sequence is an oligonucleotide modulator,
CC which targets FIXa aptamer 9.3t. FIXa aptamer binds to human coagulation
CC Factor IXa and was used to illustrate the method of the invention. This
CC oligonucleotide was found to be effective at reversing FIXa aptamer's
CC anticoagulation activity in human plasma in vitro
XX SQ Sequence 18 BP; 5 A; 3 C; 7 G; 0 T; 3 U; 0 Other;
Query Match 50.0%; Score 17; DB 7; Length 18;
Best Local Similarity 70.6%; Pred. No. 4.3e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 18 UAAUGCGUCGUCCCAU 34
Db :||:||||:|||||
18 TAATGCTGCTCCCAT 2
Search completed: April 9, 2004, 03:17:46
Job time : 122.8 secs
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 02:54:20 ; Search time 27.8667 Seconds
(without alignments)
677.093 Million cell updates/sec

Title: US-09-963-827B-70
Perfect score: 34
Sequence: 1 auggggacuaaccgnaauggcuccccau 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 979464

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Issued Patents NA:
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6: /cgn2_6/prodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.2	50.6	115	4	US-09-621-976-13765 Sequence 13765, A
2	17.2	50.6	196	4	US-09-643-597-317 Sequence 317, App
3	17.2	50.6	196	4	US-09-480-884A-317 Sequence 317, App
4	17.2	50.6	196	4	US-09-542-615A-317 Sequence 317, App
5	17.2	50.6	196	4	US-09-606-421B-317 Sequence 317, App
6	17	50.0	46	2	US-08-448-267A-6 Sequence 6, Appli
7	15.4	45.3	38	4	US-09-474-432B-1341 Sequence 1341, Ap
8	15.4	45.3	38	4	US-09-476-387-1340 Sequence 1340, Ap
9	15.4	45.3	147	4	US-09-536-094-2 Sequence 2, Appli
10	15.4	45.3	183	4	US-09-134-001C-282 Sequence 282, App
11	15	44.1	117	4	US-09-313-294A-6423 Sequence 6423, Ap
12	14.8	43.5	46	4	US-09-486-241-1 Sequence 1, Appli
13	14.8	43.5	94	4	US-08-585-593A-18 Sequence 18, Appl
14	14.8	43.5	130	4	US-08-956-171E-2861 Sequence 2861, Ap
15	14.6	42.9	50	4	US-09-168-947-9 Sequence 9, Appli
16	14.6	42.9	71	4	US-08-956-171B-1721 Sequence 1721, Ap
17	14.6	42.9	76	4	US-09-025-769B-134 Sequence 134, App
18	14.6	42.9	77	1	US-08-477-530-6 Sequence 6, Appli
19	14.6	42.9	77	1	US-08-477-530-6 Sequence 6, Appli
20	14.6	42.9	77	1	US-08-477-830-6 Sequence 6, Appli
21	14.6	42.9	111	4	US-09-702-705-1556 Sequence 1556, Ap
22	14.6	42.9	111	4	US-09-736-457-1556 Sequence 1556, Ap
23	14.6	42.9	111	4	US-09-614-124B-1556 Sequence 1556, Ap
24	14.6	42.9	111	4	US-09-671-325-1556 Sequence 1556, Ap
25	14.6	42.9	196	4	US-07-757-022B-21 Sequence 21, Appl
26	14.4	42.4	29	4	US-09-304-232-17 Sequence 17, Appl
27	14.4	42.4	98	1	US-08-472-255A-12 Sequence 12, Appl

c 28	14.4	42.4	98	1	US-08-479-724A-12	Sequence 12, Appl
c 29	14.4	42.4	98	3	US-08-472-256B-12	Sequence 12, Appl
c 30	14.4	42.4	98	3	US-08-952-793-12	Sequence 12, Appl
c 31	14.4	42.4	98	4	US-09-849-928-12	Sequence 12, Appl
c 32	14.4	42.4	98	5	PCT-US96-09455A-12	Sequence 12, Appl
c 33	14.4	42.4	103	3	US-08-952-664-12	Sequence 12, Appl
c 34	14.4	42.4	103	3	US-09-487-874-12	Sequence 12, Appl
c 35	14.4	42.4	142	4	US-08-956-171B-4735	Sequence 4735, Ap
c 36	14.4	42.4	189	4	US-09-621-976-18097	Sequence 18097, A
c 37	14.2	41.8	27	3	US-09-269-345-7	Sequence 7, Appli
c 38	14.2	41.8	32	1	US-08-616-133-25	Sequence 25, Appl
c 39	14.2	41.8	32	1	US-08-802-985-25	Sequence 25, Appl
c 40	14.2	41.8	39	6	5256648-11	Patent No. 5256648
c 41	14.2	41.8	45	3	US-08-675-566-34	Sequence 34, Appl
c 42	14.2	41.8	51	4	US-09-443-199C-65	Sequence 65, Appl
c 43	14.2	41.8	60	3	US-09-023-228B-126	Sequence 126, App
c 44	14.2	41.8	60	4	US-09-163-025B-126	Sequence 126, App
c 45	14.2	41.8	60	4	US-10-037-282-126	Sequence 126, App

ALIGNMENTS

RESULT 1

US-09-621-976-13765
; Sequence 13765, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13765
; LENGTH: 115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13765

Query Match 50.6%; Score 17.2; DB 4; Length 115;

Best Local Similarity 56.7%; Pred. No. 75;

Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUAACCGGUAUGGCGGCGCC 32

Db 63 GGAGATTGGACGGCCTGATGCTCCCTCCC 92

RESULT 2

US-09-643-597-317
; Sequence 317, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21

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; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 317
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-317

Query Match      50.6%; Score 17.2; DB 4; Length 196;
Best Local Similarity 56.7%; Pred. No. 84;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAUACCGGUAUAGUGCGUCUCCCC 32
Db 104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133

RESULT 3
US-09-480-884A-317
; Sequence 317, Application US/09480884A
; Patent No. 6482337
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 317
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-480-884A-317

Query Match      50.6%; Score 17.2; DB 4; Length 196;
Best Local Similarity 56.7%; Pred. No. 84;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAUACCGGUAUAGUGCGUCUCCCC 32
Db 104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133

RESULT 4
US-09-542-615A-317
; Sequence 317, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 317
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-542-615A-317

; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 317
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-317

Query Match      50.6%; Score 17.2; DB 4; Length 196;
Best Local Similarity 56.7%; Pred. No. 84;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAUACCGGUAUAGUGCGUCUCCCC 32
Db 104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133

RESULT 5
US-09-606-421B-317
; Sequence 317, Application US/09606421B
; Patent No. 6511315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 317
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-606-421B-317

Query Match      50.6%; Score 17.2; DB 4; Length 196;
Best Local Similarity 56.7%; Pred. No. 84;
Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAUACCGGUAUAGUGCGUCUCCCC 32
Db 104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133

RESULT 6
US-08-448-267A-6
; Sequence 6, Application US/08448267A
; Patent No. 5925518
; GENERAL INFORMATION:
; APPLICANT: Earle, Steven R.
; APPLICANT: Jacobson, Walter E.
; TITLE OF INVENTION: Nucleic Acid Primers for Amplification
; TITLE OF INVENTION: of a Mycobacteria RNA Template
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5925518el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,267A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
```



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QY 2 UGGGACUUAACCGGUAUAGUCGUCUCCCAU 34
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Db 104 TCTGATTACACCTCTGCTGCTCTCCCT 136
    |||||

RESULT 10
US-09-134-001C-282/c
; Sequence 282, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 282
; LENGTH: 183
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-282

Query Match 45.3%; Score 15.4; DB 4; Length 183;
Best Local Similarity 56.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 7 ACUUAACCGGUAUAGUCGUCUCC 31
    |||||
Db 177 ACAATACCTCGTATTGTGGTCGC 153
    |||||

RESULT 11
US-09-313-294A-6423
; Sequence 6423, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6423
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700351779H1
; NAME/KEY: unsure
; LOCATION: 31
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6423

Query Match 44.1%; Score 15; DB 4; Length 117;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
Matches 16; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 3 GGGACUUAACCGGUAUAGUCGUCUCCCAU 34
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Db 6 GGGGTCCATACGCGCTGTCTCGATCCCGT 37
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RESULT 12
US-09-486-241-1/c
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; Sequence 1, Application US/09486241
; Patent No. 6472184
; GENERAL INFORMATION:
; APPLICANT: Hegemann, Peter
; TITLE OF INVENTION: METHOD FOR PRODUCING NUCLEIC ACID
; TITLE OF INVENTION: POLYMERS
; FILE REFERENCE: 3910/OG706
; CURRENT APPLICATION NUMBER: US/09/486,241
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/EP98/05219
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: DE19736591.4
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-486-241-1

Query Match 43.5%; Score 14.8; DB 4; Length 46;
Best Local Similarity 55.9%; Pred. No. 7.8e+02;
Matches 19; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 AUGGGACUUAACCGGUAUAGUCGUCUCCCAU 34
    |||||
Db 41 ATGGGGACACACCGGTGAACAGCTCTCTCGCCT 8
    |||||

RESULT 13
US-08-585-593A-18
; Sequence 18, Application US/08585593A
; Patent No. 6503706
; GENERAL INFORMATION:
; APPLICANT: ABKEN, Hinrich J
; APPLICANT: ALBERT, Winfried
; APPLICANT: JUNGFER, Herbert
; TITLE OF INVENTION: METHOD OF IDENTIFYING HUMAN AND ANIMAL
; TITLE OF INVENTION: CELLS CAPABLE OF UNLIMITED PROLIFERATION OR TUMOR
; TITLE OF INVENTION: FORMATION
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,593A
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP94/02307
; FILING DATE: 13-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 23 727.4
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 18:
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SEQUENCE CHARACTERISTICS:
LENGTH: 94 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-585-593A-18

Query Match 43.5%; Score 14.8; DB 4; Length 94;
Best Local Similarity 57.7%; Pred. No. 9e+02;
Matches 15; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 5 GGACUUAACGGGUAUGCGCCUCC 30
DB 52 GGGCTGCACAGAAATCTGCTCC 77

RESULT 14
US-08-956-171E-2661
Sequence 2661, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:

APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 2661:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2661:

US-08-956-171E-2661

Query Match 43.5%; Score 14.8; DB 4; Length 130;
Best Local Similarity 50.0%; Pred. No. 9.6e+02;
Matches 17; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 AUGGGGACUUAACGGGUAUGCGCCUCCAU 34
:|||||:|||||:|||||:|||||:

Db 12 ATGGGGTAATTTCCGCCAAATCCCGTTTCCCCCT 45

RESULT 15
US-09-168-947-9
Sequence 9, Application US/09168947
Patent No. 6589734
GENERAL INFORMATION:
APPLICANT: KACIAN, DANIEL L.
APPLICANT: FULTZ, TIMOTHY J.
APPLICANT: MCDONOUGH, SHERROL H.
TITLE OF INVENTION: DETECTION OF HIV
FILE REFERENCE: 218/130
CURRENT APPLICATION NUMBER: US/09/168,947
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 08/469,067
EARLIER FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 07/550,837
EARLIER FILING DATE: 1990-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized nucleic acid molecule
US-09-168-947-9

Query Match 42.9%; Score 14.6; DB 4; Length 50;
Best Local Similarity 55.2%; Pred. No. 9.8e+02;
Matches 16; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 AUGGGGACUUAACGGGUAUGCGCCUC 29
DB 21 AGGGAGACTCCCCCTTAATCTAGCG 49

Search completed: April 9, 2004, 06:07:34
Job time : 29.8667 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 03:53:35 ; Search time 420.8 Seconds
(without alignments)
303.112 Million cell updates/sec

Title: US-09-963-827B-70
Perfect score: 34
Sequence: 1 augggagcuauaccgcuauugcuccccau 34

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 247585 seqs, 1875730760 residues
Total number of hits satisfying chosen parameters: 1817818

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PTVUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09D_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	10	US-09-963-827B-70
2	34	100.0	35	14	US-10-155-233-1
3	34	100.0	35	14	US-10-155-233-19
4	34	100.0	40	14	US-10-155-233-2
5	34	100.0	96	10	US-09-963-827B-3
6	21	61.8	23	14	US-10-155-233-29
7	17.2	50.6	196	9	US-09-735-705-317
8	17.2	50.6	196	9	US-09-850-716A-317
9	17.2	50.6	196	9	US-09-897-778-317
10	17.2	50.6	196	14	US-10-117-982-317
11	17.2	50.6	196	15	US-10-113-986-317
12	17	50.0	17	14	US-10-155-233-25
13	17	50.0	17	14	US-10-155-233-41
14	17	50.0	18	14	US-10-155-233-26
15	17	50.0	20	14	US-10-155-233-20

c	16	17	50.0	112	9	US-09-864-761-22160	Sequence 22160, A
	17	16.6	48.8	66	15	US-10-027-632-178287	Sequence 178287, A
	18	16.6	48.8	66	15	US-10-027-632-178289	Sequence 178289, A
c	19	16.6	48.8	200	10	US-09-814-353-13516	Sequence 13516, A
	20	16.4	48.2	161	15	US-10-027-632-178667	Sequence 178667, A
c	21	16.4	48.2	199	12	US-10-085-783A-15330	Sequence 15330, A
	22	16.4	48.2	199	15	US-10-242-535A-15330	Sequence 15330, A
c	23	16.2	47.6	113	9	US-09-864-761-27147	Sequence 27147, A
	24	15.6	45.9	33	14	US-10-155-233-18	Sequence 18, Appl
	25	15.6	45.9	76	9	US-09-815-243-805	Sequence 805, Appl
	26	15.6	45.9	76	12	US-10-282-122A-775	Sequence 775, Appl
	27	15.6	45.9	164	9	US-09-864-761-18483	Sequence 18483, A
c	28	15.4	45.3	38	10	US-09-825-805-1340	Sequence 1340, Appl
	29	15.4	45.3	64	10	US-09-766-880B-16	Sequence 16, Appl
c	30	15.4	45.3	147	9	US-09-977-432-2	Sequence 2, Appl
	31	15.4	45.3	147	9	US-09-961-563-2	Sequence 2, Appl
	32	15.4	45.3	147	13	US-10-014-220-2	Sequence 2, Appl
	33	15.4	45.3	162	12	US-10-085-783A-626	Sequence 626, Appl
c	34	15.4	45.3	162	15	US-10-242-535A-626	Sequence 626, Appl
	35	15.4	45.3	190	9	US-09-864-761-31632	Sequence 31632, A
	36	15.2	44.7	105	9	US-09-896-915-38	Sequence 38, Appl
c	37	15.2	44.7	121	10	US-09-818-875-1097	Sequence 1097, Appl
	38	15.2	44.7	121	10	US-09-818-875-1098	Sequence 1098, Appl
c	39	15.2	44.7	121	15	US-10-209-787-1097	Sequence 1097, Appl
	40	15.2	44.7	121	15	US-10-209-787-1098	Sequence 1098, Appl
c	41	15.2	44.7	121	15	US-10-261-185-1097	Sequence 1097, Appl
	42	15.2	44.7	121	15	US-10-261-185-1098	Sequence 1098, Appl
	43	15.2	44.7	130	12	US-10-424-599-30668	Sequence 30668, A
c	44	15.2	44.7	137	12	US-10-424-599-41653	Sequence 41653, A
	45	15.2	44.7	152	12	US-10-424-599-133545	Sequence 133545, A

ALIGNMENTS

RESULT 1
US-09-963-827B-70
; Sequence 70, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Sullenger, Bruce
; APPLICANT: Rusconi, Christopher
; TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
; FILE REFERENCE: 180/124/2
; CURRENT APPLICATION NUMBER: US/09/963,827B
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,654
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RNA aptamer
; NAME/KEY: misc_feature
; LOCATION: (1)..(34)
; OTHER INFORMATION: RNA aptamer
US-09-963-827B-70

Query Match 100.0%; Score 34; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AUGGGAGCUAUACCGCUAUUGCUCGCCCAU 34
Db 1 AUGGGAGCUAUACCGCUAUUGCUCGCCCAU 34
RESULT 2

US-10-155-233-1
; Sequence 1, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
; APPLICANT: SULLENGER, BRUCE A
; TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
; FILE REFERENCE: 1579-684
; CURRENT APPLICATION NUMBER: US/10/155,233
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,231
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/331,037
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 35
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Aptamer
; NAME/KEY: misc_RNA
; LOCATION: (35)-
; OTHER INFORMATION: N=1dt
US-10-155-233-1

Query Match 100.0%; Score 34; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUGGGGACUUAACCGGUAUAGCUGCCUCCCAU 34
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DB 1 AUGGGGACUUAACCGGUAUAGCUGCCUCCCAU 34

RESULT 3
US-10-155-233-19
; Sequence 19, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
; APPLICANT: SULLENGER, BRUCE A
; TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
; FILE REFERENCE: 1579-684
; CURRENT APPLICATION NUMBER: US/10/155,233
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,231
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/331,037
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 35
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Aptamer
; NAME/KEY: misc_RNA
; LOCATION: (27)-
; OTHER INFORMATION: N=mGmUmC1dt
US-10-155-233-19

Query Match 100.0%; Score 34; DB 14; Length 35;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUGGGGACUUAACCGGUAUAGCUGCCUCCCAU 34
|||||
DB 1 AUGGGGACUUAACCGGUAUAGCUGCCUCCCAU 34

RESULT 4
US-10-155-233-2
; Sequence 2, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
; APPLICANT: SULLENGER, BRUCE A
; TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
; FILE REFERENCE: 1579-684
; CURRENT APPLICATION NUMBER: US/10/155,233
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,231
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/331,037
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 40
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Aptamer
US-10-155-233-2

Query Match 100.0%; Score 34; DB 14; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUGGGGACUUAACCGGUAUAGCUGCCUCCCAU 34
|||||
DB 4 AUGGGGACUUAACCGGUAUAGCUGCCUCCCAU 37

RESULT 5
US-09-963-827B-3
; Sequence 3, Application US/09963827B
; Publication No. US20030175703A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: SULLENGER, BRUCE
; APPLICANT: RUSCONI, CHRISTOPHER
; TITLE OF INVENTION: RNA APTAMERS AND METHODS FOR IDENTIFYING THE SAME
; FILE REFERENCE: 180/124/2
; CURRENT APPLICATION NUMBER: US/09/963,827B
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,654
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 96
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RNA aptamer
; NAME/KEY: RNA aptamer
; LOCATION: (1)-(96)
; OTHER INFORMATION: RNA aptamer
US-09-963-827B-3

Query Match 100.0%; Score 34; DB 10; Length 96;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUGGGGACUUAACCGGUAUAGCUGCCUCCCAU 34
|||||
DB 18 AUGGGGACUUAACCGGUAUAGCUGCCUCCCAU 51

RESULT 6
 US-10-155-233-29/c
 ; Sequence 29, Application US/10155233
 ; Publication No. US20030083294A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SULLENGER, BRUCE A
 ; APPLICANT: RUSCONI, CHRISTOPHER
 ; TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
 ; FILE REFERENCE: 1579-684
 ; CURRENT APPLICATION NUMBER: US/10/155,233
 ; CURRENT FILING DATE: 2002-05-28
 ; PRIOR APPLICATION NUMBER: 60/293,231
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/331,037
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 29
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Aptamer
 US-10-155-233-29

Query Match 61.8%; Score 21; DB 14; Length 23;
 Best Local Similarity 81.0%; Pred. No. 6.4;
 Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGGACUUAUACCGGUAAUGC 23
 |||||:||||:||||:||||:
 DB 21 GGGGACTATACCGGTAATGC 1

RESULT 7
 US-09-735-705-317
 ; Sequence 317, Application US/09735705
 ; Patent No. US20020052329A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Fanger, Neil
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.455C14
 ; CURRENT APPLICATION NUMBER: US/09/735,705
 ; CURRENT FILING DATE: 2000-12-12
 ; NUMBER OF SEQ ID NOS: 419
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 317
 ; LENGTH: 196
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-735-705-317

Query Match 50.6%; Score 17.2; DB 9; Length 196;
 Best Local Similarity 56.7%; Pred. No. 4.6e+02;
 Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAUACCGGUAAUGCUCUCCCC 32
 |||||:||||:||||:||||:
 DB 104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133

RESULT 8
 US-09-850-716A-317
 ; Sequence 317, Application US/09850716A
 ; Patent No. US20020115139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Retter, Marc W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.455C15
 ; CURRENT APPLICATION NUMBER: US/09/850,716A
 ; CURRENT FILING DATE: 2001-05-07
 ; NUMBER OF SEQ ID NOS: 440
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 317
 ; LENGTH: 196
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-850-716A-317

Query Match 50.6%; Score 17.2; DB 9; Length 196;
 Best Local Similarity 56.7%; Pred. No. 4.6e+02;
 Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAUACCGGUAAUGCUCUCCCC 32
 |||||:||||:||||:||||:
 DB 104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133

RESULT 9
 US-09-897-778-317
 ; Sequence 317, Application US/09897778
 ; Patent No. US20020147143A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Marnerakis, Margarita
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Peckham, David W.
 ; APPLICANT: Fanger, Neil
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.455C16
 ; CURRENT APPLICATION NUMBER: US/09/897,778
 ; CURRENT FILING DATE: 2001-06-28
 ; NUMBER OF SEQ ID NOS: 467
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 317
 ; LENGTH: 196
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-897-778-317

Query Match 50.6%; Score 17.2; DB 9; Length 196;
 Best Local Similarity 56.7%; Pred. No. 4.6e+02;
 Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGGACUUAUACCGGUAAUGCUCUCCCC 32
 |||||:||||:||||:||||:
 DB 104 GGAGATTGGACGGCCTGATGCTCCCTCCCC 133

RESULT 10
 US-10-117-982-317
 ; Sequence 317, Application US/10117982
 ; Publication No. US20030138438A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Foy, Teresa M.
 ; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Mericle, Barbara
 ; APPLICANT: Spies, Gregory A.
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Wang, Tongtong
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.455C18
 ; CURRENT APPLICATION NUMBER: US/10/117,982
 ; CURRENT FILING DATE: 2002-04-05
 ; NUMBER OF SEQ ID NOS: 484
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 317
 ; LENGTH: 196
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-117-982-317

Query Match 50.6%; Score 17.2; DB 14; Length 196;
 Best Local Similarity 56.7%; Pred. No. 4.6e+02;
 Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGACUAUACCGGUAUGCGUCCGCC 32
 DB 104 GGAGATTGACGGCGTGATGCTCCCTCC 133

RESULT 11
 US-10-313-986-317
 ; Sequence 317, Application US/10313986
 ; Publication No. US20030236209A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FOY, Teresa M.
 ; APPLICANT: McNabb, Andria
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Wang, Tongtong
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.455C19
 ; CURRENT APPLICATION NUMBER: US/10/313,986
 ; CURRENT FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 560
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 317
 ; LENGTH: 196
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-313-986-317

Query Match 50.6%; Score 17.2; DB 15; Length 196;
 Best Local Similarity 56.7%; Pred. No. 4.6e+02;
 Matches 17; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 3 GGGACUAUACCGGUAUGCGUCCGCC 32
 DB 104 GGAGATTGACGGCGTGATGCTCCCTCC 133

RESULT 12
 US-10-155-233-25/c
 ; Sequence 25, Application US/10155233
 ; Publication No. US20030083294A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SULLENGER, BRUCE A
 ; APPLICANT: RUSCONI, CHRISTOPHER
 ; TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
 ; FILE REFERENCE: 1579-684
 ; CURRENT APPLICATION NUMBER: US/10/155,233

; CURRENT FILING DATE: 2002-05-28
 ; PRIOR APPLICATION NUMBER: 60/293,231
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/331,037
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 25
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Aptamer
 US-10-155-233-25

Query Match 50.0%; Score 17; DB 14; Length 17;
 Best Local Similarity 70.6%; Pred. No. 4.3e+02;
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 18 UAAUGCUGCCUCCCAU 34
 DB 17 TAATGCTGCTCCCAT 1

RESULT 13
 US-10-155-233-41/c
 ; Sequence 41, Application US/10155233
 ; Publication No. US20030083294A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SULLENGER, BRUCE A
 ; APPLICANT: RUSCONI, CHRISTOPHER
 ; TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
 ; FILE REFERENCE: 1579-684
 ; CURRENT APPLICATION NUMBER: US/10/155,233
 ; CURRENT FILING DATE: 2002-05-28
 ; PRIOR APPLICATION NUMBER: 60/293,231
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/331,037
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 41
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:Aptamer
 US-10-155-233-41

Query Match 50.0%; Score 17; DB 14; Length 17;
 Best Local Similarity 82.4%; Pred. No. 4.3e+02;
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AUGGGACUAUACCGCG 17
 DB 17 ATGGGACTATACCGG 1

RESULT 14
 US-10-155-233-26/c
 ; Sequence 26, Application US/10155233
 ; Publication No. US20030083294A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SULLENGER, BRUCE A
 ; APPLICANT: RUSCONI, CHRISTOPHER
 ; TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
 ; FILE REFERENCE: 1579-684
 ; CURRENT APPLICATION NUMBER: US/10/155,233
 ; CURRENT FILING DATE: 2002-05-28
 ; PRIOR APPLICATION NUMBER: 60/293,231
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/331,037
 ; PRIOR FILING DATE: 2001-11-07

```

; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Aptamer
US-10-155-233-26

```

```

Query Match          50.0%; Score 17; DB 14; Length 18;
Best Local Similarity 70.6%; Pred. No. 4.3e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 18 UAAUGCUGCCUCCCAU 34
    :||:||||:||||:
DB 18 TAATGCTGCTCCCAT 2

```

```

RESULT 15
US-10-155-233-20/c
; Sequence 20, Application US/10155233
; Publication No. US20030083294A1
; GENERAL INFORMATION:
; APPLICANT: SULLENGER, BRUCE A
; APPLICANT: RUSCONI, CHRISTOPHER
; TITLE OF INVENTION: MODULATORS OF PHARMACOLOGICAL AGENTS
; FILE REFERENCE: 1579-684
; CURRENT APPLICATION NUMBER: US/10/155,233
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,231
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/331,037
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Aptamer
US-10-155-233-20

```

```

Query Match          50.0%; Score 17; DB 14; Length 20;
Best Local Similarity 70.6%; Pred. No. 4.4e+02;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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QY 18 UAAUGCUGCCUCCCAU 34
    :||:||||:||||:
DB 20 TAATGCTGCTCCCAT 4

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Search completed: April 9, 2004, 10:11:30
 Job time : 420.8 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 02:50:24 ; Search time 1040.4 Seconds
(without alignments)
975.888 Million cell updates/sec

Title: US-09-963-827B-70

Perfect score: 34

Sequence: 1 augggacuaacccgcgaugcuccccau 34

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 3354136

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_esti:*

9: gb_esti:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gesl:*

29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.4	57.1	108	29	CG733695 1119158F0
2	19.4	57.1	108	29	CG733696 1119158F0
3	18.8	55.3	179	10	BE183096 CM2-HT065
4	18.8	55.3	188	10	AW997328 RC2-BN004

C	5	18.6	54.7	145	9	AI873178	AI873178 wc47f02.x
C	6	18.6	54.7	175	12	BI781660	BI781660 kh15d01.Y
C	7	18	52.9	92	13	BU648134	BU648134 1112066D1
C	8	18	52.9	175	9	AA249214	AA249214 hfe0270.6
C	9	17.8	52.4	194	9	AV011213	AV011213 AV011213
C	10	17.6	51.8	119	28	AZ258888	AZ258888 RPCI-23-1
C	11	17.6	51.8	127	28	AZ121703	AZ121703 RPCI-23-4
C	12	17.6	51.8	168	10	BB170705	BB170705 BB170705
C	13	17.4	51.2	97	29	CG613410	CG613410 OST300555
C	14	17.4	51.2	160	14	CK296959	CK296959 EST759673
C	15	17.2	50.6	56	28	AZ512563	AZ512563 1M0358G13
C	16	17.2	50.6	80	13	BQ818470	BQ818470 1030071B0
C	17	17.2	50.6	107	13	BQ319143	BQ319143 PM4-CT056
C	18	17.2	50.6	111	13	BQ824632	BQ824632 1030120B0
C	19	17.2	50.6	138	12	BI998642	BI998642 1031060A1
C	20	17.2	50.6	143	12	BI022472	BI022472 CW3-MT034
C	21	17.2	50.6	149	9	AV390541	AV390541 AV390541
C	22	17.2	50.6	155	13	BQ808240	BQ808240 1030002G0
C	23	17.2	50.6	160	13	BQ824080	BQ824080 1030115F0
C	24	17.2	50.6	161	13	BQ822227	BQ822227 1030099C0
C	25	17.2	50.6	162	12	BI996058	BI996058 1031032H0
C	26	17.2	50.6	162	13	BQ824649	BQ824649 1030120C0
C	27	17.2	50.6	163	10	AW146518	AW146518 ME000480.
C	28	17.2	50.6	163	13	BQ809459	BQ809459 1030011C0
C	29	17.2	50.6	172	12	BI997268	BI997268 1031048F0
C	30	17.2	50.6	175	13	BQ811695	BQ811695 1030025A0
C	31	17.2	50.6	177	13	BQ824879	BQ824879 1030122A0
C	32	17.2	50.6	178	12	BI720254	BI720254 1031048F0
C	33	17.2	50.6	185	12	BI816617	BI816617 1031063A1
C	34	17.2	50.6	187	28	AZ372216	AZ372216 1M0124A05
C	35	17.2	50.6	188	28	BZ970131	BZ970131 PUGGX387B
C	36	17.2	50.6	196	13	BQ825311	BQ825311 1030125H0
C	37	17.2	50.6	199	13	BQ821049	BQ821049 1030088H1
C	38	17	50.0	107	14	CF296285	CF296285 30DGS--06
C	39	17	50.0	165	28	AQ304066	AQ304066 HS_3211.B
C	40	17	50.0	188	28	BH086749	BH086749 RPCI-24-3
C	41	16.8	49.4	181	10	BF914058	BF914058 RCI-UT008
C	42	16.8	49.4	181	12	BM846477	BM846477 K-EST0125
C	43	16.8	49.4	196	10	BF956024	BF956024 RC3-NN118
C	44	16.6	48.8	85	9	AI001002	AI001002 O846g11.8
C	45	16.6	48.8	102	12	BI039685	BI039685 IL3-NT028

ALIGNMENTS

RESULT 1	CG733695	1119158F02.2EL.x1	1119	- RescueMu Grid AA	linear	GSS 20-OCT-2003
LOCUS	CG733695	survey sequence.	108 bp	DNA		
DEFINITION	CG733695	CG733695.1	GI:37776187			
ACCESSION	CG733695					
VERSION	GSS.					
KEYWORDS	CG733695.1					
SOURCE	Zea mays					
ORGANISM	Zea mays					
REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.					
AUTHORS	Walbot,V.					
TITLE	Maize genomic sequences found using engineered RescueMu transposon					
JOURNAL	Unpublished (2001)					
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence. Plate: 1119158 row: 8					

```

Class: transposon-tagged.
Location/Qualifiers
1..108
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stages="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match 57.1%; Score 19.4; DB 29; Length 108;
Best Local Similarity 65.5%; Pred. No. 9.7e+02;
Matches 19; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 5 GGACUAUACCGCGUAAGCUGCCUCCCA 33
|||:|||||:|||||:|||||:|||||
DB 8 GAATCTACCGCGCATGCTGCCGCTCA 36

RESULT 3
BE183096
LOCUS BE183096 179 bp mRNA linear EST 22-JUN-2000
DEFINITION CM2-HT0655-170400-157-h05 HT0655 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE183096
VERSION BE183096.1 GI:8662272
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-CM2-HT0655-170
400-157-h05&t3=2000-04-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 36
High quality sequence stop: 178.
Location/Qualifiers
1..179
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stages="Adult"
/clone_lib="HT0655"
/note="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under

```


low stringency conditions."

ORIGIN

Query Match 55.3%; Score 18.8; DB 10; Length 179;
Best Local Similarity 56.7%; Pred. No. 2e+03;
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 UGGGACUAAUACCGGUAAUGCGUCCUCC 31
:|||||: : ||||| : ||||| : ||||| : ||||| :
Db 61 TGGGTACTTTGGCGCGCGCGTCTGCTTCC 90

RESULT 4

AW997328/c
LOCUS 188 bp mRNA linear EST 05-JUN-2000
DEFINITION RC2-BN0048-250400-019-h08 BN0048 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW997328
VERSION AW997328.1 GI:8257562
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188)

AUTHORS Dias Neco, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC2-BN0048-250400-019-h08&t3=2000-04-25&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 188.

Location/Qualifiers

FEATURES

source

1..188
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0048"

/note="Organ: breast normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 55.3%; Score 18.8; DB 10; Length 188;
Best Local Similarity 63.3%; Pred. No. 2e+03;
Matches 19; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGGACUAAUACCGGUAAUGCGUCCUCCCA 33
:|||||: : ||||| : ||||| : ||||| : ||||| :
Db 57 GGGACCGTACCAAGGCTGCTGCTCACCA 28

RESULT 5

AI873178/c

LOCUS 145 bp mRNA linear EST 17-DEC-1999

DEFINITION wc47f02.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2321787 3',

mRNA sequence.

AI873178

VERSION AI873178.1 GI:5547227

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 145)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: Washington University Genome Sequencing Center

NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert length: 760 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 142.

Location/Qualifiers

1..145

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2321787"

/sex="male"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Pr28"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)

with a modified polylinker; Plasmid DNA from the

normalized library NCI CGAP Pr22 was prepared, and as

circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (clonids

985608-986759, 1101192-1101959, and 1217928-1220615).

Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 54.7%; Score 18.6; DB 9; Length 145;

Best Local Similarity 54.5%; Pred. No. 2.3e+03;

Matches 18; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 AUGGGGACUAAUACCGGUAAUGCGUCCCA 33

:|||||: : ||||| : ||||| : ||||| : ||||| :

Db 44 ATGCGGAATCTCCGAGTGATGCGGCTCCCA 12

RESULT 6

BI781660/c

LOCUS 175 bp mRNA linear EST 26-SEP-2001

DEFINITION Kh15d01.Y1 Ascaris suum female gonad MZ pAMPl v2 Chiapelli McCarter

Ascaris suum cDNA 5', mRNA sequence.

BI781660

VERSION BI781660.1 GI:15784552

KEYWORDS EST.

SOURCE Ascaris suum (pig roundworm)

ORGANISM Ascaris suum

Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;


```
Fax: 6179750995
Email: cliw@rics.bwh.harvard.edu
PCR Primers
FORWARD: 5' GCCAAGCTCGAAATTAACCTCTCACTAAAGG 3'
BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGCG 3'
Seq primer: 5' GAAATTAACCTCTCACTAAAGG 3'

FEATURES
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        Location/Qualifiers
            1..175
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /lab_host="E. coli XL1-Blue"
                /clone_lib="Human fetal heart, Lambda ZAP Express"
                /notes="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
                XhoI; mRNA was purified from human fetal hearts (8-10
                weeks). cDNA was synthesized using a XhoI-Oligo dT
                adaptor-primer. EcoRI adaptors were ligated, followed by
                digestion with XhoI, for directional cloning into
                predigested lambda ZAP Express."

ORIGIN
    Query Match      52.9%; Score 18; DB 9; Length 175;
    Best Local Similarity 50.0%; Pred. No. 4.3e+03;
    Matches 17; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 AUGGGACUAUACCGCUAUAUGCGUCUCCCAU 34
    ||||| :||| :||| :||| :||| :
Db 7 ATGGGGTCCATACGGCGTGTCTGCGATTCCTCGT 40

RESULT 9
AV011213/c
LOCUS
DEFINITION
    194 bp mRNA linear EST 25-AUG-1999
AV011213 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA
clone 1110030P07, mRNA sequence.

ACCESSION
AV011213
VERSION
AV011213.1 GI:4788200
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 194)
Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,
Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,
Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H.,
Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,
Sugahara,Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y.,
Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T.,
Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-resortc.riken.go.jp
Thermotabilization and thermostactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
    Location/Qualifiers
        1..194
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"

FEATURES
    source
        Location/Qualifiers
            1..119
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="RPCI-23-11211"
                /sex="Female"
                /lab_host="DH10B"
                /clone_lib="RPCI-23"
                /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1:
                EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
                brain genomic DNA was isolated and partially digested
                with a combination of EcoRI and EcoRI Methylase. Size
                selected DNA was cloned into the pBAC3.6 vector at the
                EcoRI sites. The ligation products were transformed into
                DH10B electrocompetent cells (BRL Life Technologies). "
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/clone="1110030P07"
/sex="mixed"
/dev_stage="18-day embryo"
/clone_lib="Mus musculus 18-day embryo C57BL/6J"

ORIGIN
    Query Match      52.4%; Score 17.8; DB 9; Length 194;
    Best Local Similarity 58.6%; Pred. No. 5.4e+03;
    Matches 17; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 5 GGCAUAUACCGCUAUAUGCGUCUCCCA 33
    ||| :||| :||| :||| :||| :
Db 63 GGAATTATCCGAAATGCTTGTCTCCCA 35

RESULT 10
AZ258888/c
LOCUS
DEFINITION
    119 bp DNA linear GSS 26-JUL-2000
AZ258888 RPCI-23-11211.TV RPCI-23 Mus musculus genomic clone RPCI-23-11211,
genomic survey sequence.

ACCESSION
AZ258888
VERSION
AZ258888.1 GI:9464812
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 119)
Zhao,S., Niernan,W., Feldblyum,T., Malek,J., Shatsman,S., de
Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-11211.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@bigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 112 row: 1 column: 1
Seq primer: T7
Class: BAC ends.

FEATURES
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        Location/Qualifiers
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="RPCI-23-11211"
                /sex="Female"
                /lab_host="DH10B"
                /clone_lib="RPCI-23"
                /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1:
                EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
                brain genomic DNA was isolated and partially digested
                with a combination of EcoRI and EcoRI Methylase. Size
                selected DNA was cloned into the pBAC3.6 vector at the
                EcoRI sites. The ligation products were transformed into
                DH10B electrocompetent cells (BRL Life Technologies). "
```

ORIGIN

```
Query Match      51.8%; Score 17.6; DB 28; Length 119;
Best Local Similarity 53.1%; Pred. No. 5.7e+03;
Matches 17; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
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ACCESSION	CK296959
VERSION	CK296959.1
GI	39802864

**JOURNAL
COMMENT**

Unpublished (2000)
Contact: Robert B. Weiss

FEATURES	Location/Qualifiers
source	1. . 56
high quality sequence stop:	30

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1. .56
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0358G13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GII4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match	50.6%	Score 17.2;	DB 28;	Length 56;
Best Local Similarity	63.6%;	Pred. No. 6.7e+03;		
Matches 14;	Conservative	5;	Mismatches 3;	Indels 0;
				Gaps 0;

QY 13 CCGCGUAAUGCUGCCUCCCCAU 34
| | | | | : | | | | :
Db 24 CAGAGTAATCCTGCCTCCCCAT 3

Search completed: April 9, 2004, 06:03:59
Job time : 1044.9 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2004, 01:42:24 ; Search time 241.439 Seconds
(without alignments)
5206.064 Million cell updates/sec

Title: US-09-963-827B-71
Perfect score: 29
Sequence: 1 ggggacuaacggcaacugcaucccc 29

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 2199298

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.ste.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pin.*
- 35: em.htg_rod.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	65.5	169	6	AR051528 Sequence
C 2	19	65.5	169	6	AR072668 Sequence
C 3	19	65.5	169	6	AR073213 Sequence
C 4	17.8	61.4	101	11	G43342 Sequence
C 5	16.8	57.9	166	6	AX923424 Sequence
C 6	16.8	57.9	181	6	AX923425 Sequence
C 7	16.4	56.6	160	11	AB059077 Sus scrofa
C 8	16	55.2	51	5	ECY17989
C 9	15.8	54.5	105	6	AX694803 Sequence
C 10	15.6	53.8	60	1	AF178261S1 Chlamydia
C 11	15.6	53.8	60	1	AF178265S1 Chlamydia
C 12	15.6	53.8	60	1	AF178269S1 Chlamydia
C 13	15.6	53.8	60	1	AF178273S1 Chlamydia
C 14	15.4	53.1	79	5	S67413 Xenopus lae
C 15	15.4	53.1	108	6	AX683332 Sequence
C 16	15.2	52.4	71	6	AR058826 Sequence
C 17	15.2	52.4	71	6	AR063552 Sequence
C 18	15.2	52.4	71	6	AR140942 Sequence
C 19	15.2	52.4	151	6	AX867991 Sequence
C 20	15.2	52.4	151	6	BD148053 Primer to
C 21	15.2	52.4	174	9	F320227S16 Homo sapi
C 22	15	51.7	132	9	F320227S10 Homo sapi
C 23	15	51.7	155	6	AR051547 Sequence
C 24	15	51.7	155	6	AR072687 Sequence
C 25	15	51.7	155	6	AR073232 Sequence
C 26	14.8	51.0	47	6	AR171238 Sequence
C 27	14.8	51.0	64	17	HSMC34G11 X88248 H.sapiens D
C 28	14.8	51.0	68	9	HUMTCVD1A1 L32381 Human (clon
C 29	14.6	50.3	50	6	AX164814 Sequence
C 30	14.6	50.3	94	9	AF150996 Homo sapi
C 31	14.6	50.3	105	6	BD261167 Methods f
C 32	14.6	50.3	105	6	BD273668 Protein c
C 33	14.6	50.3	105	6	BD139195 Anti-path
C 34	14.6	50.3	138	5	AB042992 Chrysophr
C 35	14.6	50.3	157	6	AX902921 Sequence
C 36	14.6	50.3	157	6	BD038454 Sequence
C 37	14.6	50.3	172	11	DM118G9T Z50272 D. melanoga
C 38	14.6	50.3	187	9	HSU15687 UI5687 Human clone
C 39	14.6	50.3	189	9	HSU15686 UI5686 Human clone
C 40	14.6	50.3	198	1	AF064198 Streptomy
C 41	14.6	50.3	198	1	AF064199 Streptomy
C 42	14.4	49.7	31	6	AX248328 Sequence
C 43	14.4	49.7	36	6	AR336716 Sequence
C 44	14.4	49.7	41	6	ARI76221 Sequence
C 45	14.4	49.7	41	6	AX003193 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR051528/c
DEFINITION Sequence 98 from patent US 5830670.
ACCESSION AR051528
VERSION AR051528.1 GI:5974892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 169)
AUTHORS de la Monte, S. and Wands, J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5830670-A 98 03-NOV-1998;

AR051528 169 bp DNA linear PAT 29-SEP-1999
Sequence 98 from patent US 5830670.

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FEATURES
  source
    Location/Qualifiers
      1..169
      /organism="unknown"
      /mol_type="unassigned DNA"
ORIGIN
  Query Match      65.5%; Score 19; DB 6; Length 169;
  Best Local Similarity 70.4%; Pred. No. 6.1e+02;
  Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 GGACUUAACCGGCAACUGGCAUCCGCC 29
    ||||| ||||| ||||| ||||| |||||
Db 36 GGACCAAGCGGCCATCGTGCCTCCCC 10
    ||||| ||||| ||||| ||||| |||||

RESULT 2
LOCUS AR072668/c 169 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 98 from patent US 5948634.
ACCESSION AR072668
VERSION AR072668.1 GI:9999432
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 169)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of alzheimer's disease
JOURNAL Patent: US 5948634-A 98 07-SEP-1999;
FEATURES
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    Location/Qualifiers
      1..169
      /organism="unknown"
      /mol_type="unassigned DNA"
ORIGIN
  Query Match      65.5%; Score 19; DB 6; Length 169;
  Best Local Similarity 70.4%; Pred. No. 6.1e+02;
  Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 GGACUUAACCGGCAACUGGCAUCCGCC 29
    ||||| ||||| ||||| ||||| |||||
Db 36 GGACCAAGCGGCCATCGTGCCTCCCC 10
    ||||| ||||| ||||| ||||| |||||

RESULT 3
LOCUS AR073213/c 169 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 98 from patent US 5948888.
ACCESSION AR073213
VERSION AR073213.1 GI:9999976
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 169)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5948888-A 98 07-SEP-1999;
FEATURES
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    Location/Qualifiers
      1..169
      /organism="unknown"
      /mol_type="unassigned DNA"
ORIGIN
  Query Match      65.5%; Score 19; DB 6; Length 169;
  Best Local Similarity 70.4%; Pred. No. 6.1e+02;
  Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 GGACUUAACCGGCAACUGGCAUCCGCC 29
    ||||| ||||| ||||| ||||| |||||
Db 36 GGACCAAGCGGCCATCGTGCCTCCCC 10
    ||||| ||||| ||||| ||||| |||||

RESULT 4
LOCUS G43342 101 bp mRNA linear STS 27-JAN-1999
DEFINITION WIAF-2007-STS Human THudson EST Homo sapiens STS cDNA, sequence tagged site.
ACCESSION G43342
VERSION G43342.1 GI:4192259
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  AUTHORS
    Wang,D.G., Fan,J.B., Siao,C.J., Berno,A., Young,P., Sapolsky,R.,
    Ghandour,G., Perkins,N., Winchester,E., Spencer,J., Kruglyak,L.,
    Stein,L., Hsie,L., Topaloglou,T., Hubbell,E., Robinson,E.,
    Mittmann,M., Morris,M.S., Shen,N., Kilburn,D., Rioux,J.,
    Nusbaum,C., Rozen,S., Hudson,T.J., Lipshutz,R., Chee,M. and
    Lander,E.S.
  Large-scale identification, mapping, and genotyping of
  single-nucleotide polymorphisms in the human genome
  Science 280 (5366), 1077-1082 (1998)
  98248615
  9582121
  Synonyms: CL_EST232115
  Contact: Thomas Hudson
  Whitehead Institute/MIT Center for Genome Research
  Whitehead Institute for Biomedical Research
  9 Cambridge Center, Cambridge MA 02142 USA
  Tel: 617 252 1900
  Fax: 617 252 1902
  Email: thudson@genome.wi.mit.edu
  Primer A: TAAACATACGACTACTGTACACG
  Primer B: TCCCTCTCGATATACACG
  STS size: 101
  PCR Profile:
    Presoak: 94 degrees C for 4.00 minutes
    Denaturation: 94 degrees C for 50.0 seconds
    Annealing: 58 degrees C for 1.50 minutes
    Polymerization: 72 degrees C for 1.00 minutes
    PCR Cycles: 30
    Thermal Cycler: custom built by IAS, Costar, Cambridge MA
  Protocol:
    Template: 10 ng
    Primer: each 5 pM
    dNTPs: 4 nM
    Taq Polymerase: 0.5 U
    Total Vol: 20 uL
  Buffer:
    Mg2+: 1.5 mM
    KCl: 50 mM
    Tris-HCl: 10 mM
    Gelatin: .001 %
    Location/Qualifiers
      1..101
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /mag="147.90 cR from top of Chr1 linkage group"
      /clone_lib="Human THudson EST"
      /note="STS derived from sequences in dbEST and the
      UniGene collection."
      1..101
      1..25
      complement(81..101)
    primer_bind
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ORIGIN
  Query Match 61.4%; Score 17.8; DB 11; Length 101;
  Best Local Similarity 62.1%; Pred. No. 2.3e+03;
  Matches 18; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
```



```

QY 1 GGGGACUUAUACCGGCAUUCGUGCAUCC 29
| | | | | : | | | | | : | | | | |
Db 11 GAGTACTGTACACGCAATGCGTCATGCC 39

RESULT 5
AX923424
LOCUS AX923424 166 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from Patent WO03080816.
ACCESSION AX923424
VERSION AX923424.1 GI:40216473
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Andrews, P. and Draper, J.
TITLE Stem cell culture
JOURNAL Patent: WO 03080816-A 1 02-OCT-2003;
THE UNIVERSITY OF SHEFFIELD (GB)
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Query Match 57.9%; Score 16.8; DB 6; Length 166;
Best Local Similarity 60.7%; Pred. No. 6.9e+03;
Matches 17; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGACUUAUACCGGCAUUCGUGCAUCC 28
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Db 67 GGGGACTATCCCGCACCGTGGCTGCC 94

RESULT 6
AX923425
LOCUS AX923425 181 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from Patent WO03080816.
ACCESSION AX923425
VERSION AX923425.1 GI:40216474
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Andrews, P. and Draper, J.
TITLE Stem cell culture
JOURNAL Patent: WO 03080816-A 2 02-OCT-2003;
THE UNIVERSITY OF SHEFFIELD (GB)
FEATURES
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Best Local Similarity 60.7%; Pred. No. 6.9e+03;
Matches 17; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGACUUAUACCGGCAUUCGUGCAUCC 28
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Db 67 GGGGACTATCCCGCACCGTGGCTGCC 94

RESULT 7
AB059077
LOCUS AB059077 160 bp DNA linear STS 19-MAR-2002
DEFINITION Sus scrofa domestica genomic DNA, chromosome 10, 346B10F, sequence
tagged site.
ACCESSION AB059077
VERSION AB059077.1 GI:19570610
KEYWORDS STS.
SOURCE Sus scrofa domestica (domestic pig)
ORGANISM Sus scrofa domestica
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1
AUTHORS Kiuchi, S., Inage, Y., Hiraiwa, H., Uenishi, H. and Yasue, H.
TITLE Assignment of 280 swine genomic inserts including 31
microsatellites from BAC clones to the swine RH map (IMPRH map)
JOURNAL Mamm. Genome 13 (2), 80-88 (2002)
MEDLINE 21886643
PUBMED 11889555
REFERENCE 2 (bases 1 to 160)
AUTHORS Kiuchi, S.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2001) Sachiko Kiuchi, National Institute of
Agrobiological Sciences, Genome Research Group; 2 Ikenodai,
Kukizaki-machi, Inashiki-gun, Ibaraki 305-0901, Japan
(E-mail: sachikok@aifrc.go.jp, Tel.81-298-38-8664,
Fax:81-298-38-8674)
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Best Local Similarity 61.5%; Pred. No. 1.1e+04;
Matches 16; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 GACUUAUACCGGCAUUCGUGCAUCC 29
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RESULT 8
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LOCUS ECY17989 51 bp DNA linear VRT 29-MAR-2000
DEFINITION Enchelyopus cimbrinus mitochondrial intergenic spacer and partial
tRNA-Thr and tRNA-Pro genes.
ACCESSION Y17989
VERSION Y17989.1 GI:3717962
KEYWORDS intergenic spacer; transfer RNA-Pro; tRNA-Pro gene.
SOURCE mitochondrion Enchelyopus cimbrinus (fourbeard rockling)
ORGANISM Enchelyopus cimbrinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gaidropsaridae;
Enchelyopus.
REFERENCE 1
AUTHORS Bakke I., I., Shields, G.F. and Johansen, S.
TITLE Sequence Characterization of a Unique Intergenic Spacer in
Gadiformes Mitochondrial DNA
JOURNAL Mar. Biotechnol. 1 (5), 411-0415 (1999)
PUBMED 10525675

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REFERENCE 2 (bases 1 to 51)
AUTHORS Johansen,S.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-1998) S. Johansen, Institution University of Tromso, Tromso, Department of Molecular Cell Biology, IMB, University of Tromso, 9037 Tromso, NORWAY
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RESULT 9
AX694803/c
LOCUS AX694803 105 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 430 from Patent WO03008593.
ACCESSION AX694803
VERSION AX694803.1 GI:29417915
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Morris,D.W. and Engelhard,E.K.
TITLE Novel compositions and methods for cancer
JOURNAL Patent: WO 03008593-A 430 30-JAN-2003;
Sagres Discovery (US)
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QY 2 GGGACUAUACCGCAUUGC 20
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Db 27 GGTACTACTACTGGCAATCG 9
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RESULT 10
AF178261S1
LOCUS AF178261S1 60 bp DNA linear BCT 20-JAN-2000
DEFINITION Chlamydia trachomatis isolate CA46 major outer membrane protein (omp1) gene, variable domain 1.
ACCESSION AF178261

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VERSION AF178261.1 GI:6716621
KEYWORDS
SEGMENT 1 of 4
SOURCE Chlamydia trachomatis
ORGANISM Chlamydia trachomatis
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE 1 (bases 1 to 60)
AUTHORS Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A., Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and Kanki,P.J.
TITLE Molecular epidemiology of genital Chlamydia trachomatis infection in high-risk women in Senegal, West Africa
JOURNAL J. Clin. Microbiol. 38 (1), 138-145 (2000)
MEDLINE 20085123
PUBMED 10618077
REFERENCE 2 (bases 1 to 60)
AUTHORS Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A., Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and Kanki,P.J.
TITLE Direct Submission
JOURNAL Submitted (18-AUG-1999) Immunology and Infectious Diseases, Harvard School of Public Health, 651 Huntington Ave., Boston, MA 02115, USA
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            /note="variable domain 1"
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QY 8 AUACGGCAUUGUGCAUCCCC 29
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Db 17 ATACAGGCATAGTCGACGCTCC 38
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RESULT 11
AF178265S1
LOCUS AF178265S1 60 bp DNA linear BCT 20-JAN-2000
DEFINITION Chlamydia trachomatis isolate CA599 major outer membrane protein (omp1) gene, variable domain 1.
ACCESSION AF178265
VERSION AF178265.1 GI:6716621
KEYWORDS
SEGMENT 1 of 4
SOURCE Chlamydia trachomatis
ORGANISM Chlamydia trachomatis
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE 1 (bases 1 to 60)
AUTHORS Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A., Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and Kanki,P.J.
TITLE Molecular epidemiology of genital Chlamydia trachomatis infection in high-risk women in Senegal, West Africa
JOURNAL J. Clin. Microbiol. 38 (1), 138-145 (2000)
MEDLINE 20085123
PUBMED 10618077
REFERENCE 2 (bases 1 to 60)
AUTHORS Sturm-Ramirez,K., Brumblay,H., Diop,K., Gueye-Ndiaye,A., Sankale,J.L., Thior,I., N'Doye,I., Hsieh,C.C., Mboup,S. and Kanki,P.J.
TITLE Direct Submission
JOURNAL Submitted (18-AUG-1999) Immunology and Infectious Diseases, Harvard School of Public Health, 651 Huntington Ave., Boston, MA 02115, USA
FEATURES
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[illegible]

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OM nucleic - nucleic search, using sw model

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1195.685 Million cell updates/sec

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Gapop 10_0 , Gapext 1.0

Searched: 337863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 3774412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	29	6	ABN88558 Coagulati
2	29	100.0	29	7	ABZ21243 FIXa apta
3	29	100.0	33	7	ABZ21258 Aptamer 9
4	29	100.0	96	6	ABN88504 Coagulati
5	19	65.5	169	2	AAT27772 Human neu
6	17.8	61.4	96	6	ABN88494 Coagulati
7	17.8	61.4	101	2	AAX11804 Human bia
8	16.8	57.9	166	9	AD35061 Mouse fib
9	16.8	57.9	181	7	AD35062 Mouse fib
10	16.2	55.9	29	7	ABZ21255
11	16.2	55.9	95	6	ABN88499 Coagulati
12	16	55.2	172	7	ABX91389 Murine ge
13	15.8	54.5	50	6	ABZ01528 Human leu
14	15.8	54.5	105	8	ADA01911 Mouse car
15	15.8	54.5	105	9	ADB71650 Mouse car
16	15.6	53.8	60	1	AAN97053 Sequence
17	15.6	53.8	60	1	AAN92135 Sequence
18	15.6	53.8	60	2	AAX18012 C. tracho
19	15.6	53.8	60	6	ABK97729 C. tracho
20	15.6	53.8	60	6	ABK97792 Chlamydia
21	15.4	53.1	108	7	ACF19007 Tumour ce
22	15.4	53.1	108	7	ADC84830 MCF-7 bre
23	15.2	52.4	71	2	AAT65332 Human ker

ALIGNMENTS

RESULT 1

ID	ABN88558	ABN88558 standard; RNA; 29 BP.
XX	AC	ABN88558;
XX	AC	ABN88558;
DT	19-AUG-2002	(first entry)
XX	XX	Coagulation factor IXa (FIXa) aptamer SEQ ID NO:71.
DE	XX	RNA aptamer; identification; coagulation factor; angiotensin; thrombin;
KW	KW	E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW	KW	cell proliferation; intimal hyperplasia; angiogenesis;
XX	XX	bypass graft surgery; ss.
OS	OS	Homo sapiens.
OS	OS	Synthetic.
XX	XX	WO200226932-A2.
PN	PN	04-APR-2002.
XX	XX	26-SEP-2001; 2001WO-US030004.
PF	PF	26-SEP-2000; 2000US-0235654P.
XX	XX	(UYDU-) UNIV DUKE.
XX	XX	Sullenger BA, Rusconi CP;
XX	XX	WPI; 2002-479560/51.

Novel RNA aptamers that selectively bind coagulation pathway factors, E2F family members, Ang1 or Ang2, useful for modulating coagulation pathway factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.

Claim 14; Page 25; 216pp; English.

The present invention describes RNA aptamers (I,II,III) that selectively bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c) angiotensin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have a dissociation constant for the coagulation pathway factor, an E2F family member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have cardiant and cytostatic activities. (I) are useful for modulating the biological activity of a coagulation pathway factor which involves administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that

CC the biological activity of the coagulation pathway factor in the warm-
 CC blooded vertebrate is modulated. (I) are also useful for treating
 CC cardiovascular diseases in the mammal. (III) are useful for modulating E2F
 CC activity in a warm-blooded vertebrate. (III) are useful for modulating
 CC Angi or Ang2 activity in a warm-blooded vertebrate. (I) are potent
 CC anticoagulants and significantly delay the clotting time of normal human
 CC plasma or the activation of platelets in response to thrombin. (II) are
 CC useful for inhibiting cell proliferation in a number of conditions e.g.,
 CC intimal hyperplasia following bypass graft surgery. (III) are useful for
 CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
 CC research and therapeutic context. The aptamers are useful as diagnostic,
 CC reagents to detect the presence or absence of target substances to which
 CC they specifically bind, and for identifying substances to which they
 CC specifically bind, for isolating and purifying substances to which they
 CC bind, and as a separation reagent for retrieving the targets to which
 CC they specifically bind. ABN8488 to ABN89713 and ABH81231 represent
 CC sequences used in the exemplification of the present invention
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 SQ Sequence 29 BP; 6 A; 10 C; 8 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 29; DB 6; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.00031;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 GGGGACUAUACCGGCAUUGUGCAUCCCC 29

RESULT 2
 ABZ21243
 ID ABZ21243 standard; RNA; 29 BP.
 XX
 AC ABZ21243;
 DT 16-APR-2003 (first entry)
 XX
 DE FIXA aptamer, SEQ ID 3.
 XX
 KW Immunosuppressive; aptamer; infection; autoimmunity; tumour;
 KW inflammatory proliferative disease; hypoglycaemia; human;
 KW coagulation Factor IXa; FIXa; ss.
 XX
 OS Unidentified.

Key Location/Qualifiers
 FT misc_binding 1..5
 FT /tag= a
 FT /bound_moiety= "Nucleotides 25..29"
 FT stem_loop 14..23
 FT /tag= b
 FT misc_binding 25..29
 FT /tag= c
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WO200296926-A1.
 PN
 XX
 XX 05-DEC-2002.
 PD
 XX
 PF 28-MAY-2002; 2002WO-US016555.
 XX
 PR 25-MAY-2001; 2001US-0293231P.
 PR 07-NOV-2001; 2001US-0331037P.
 XX
 PA (UYDU-) UNIV DUKE.

Sullenger BA, Rusconi C;
 PI
 XX
 WPI; 2003-140438/13.

Altering affinity of nucleic acid ligands for target molecules in a
 patient or reversing binding of labeled ligands to target tissues, by
 administering (to a patient receiving the ligand) a modulator that binds

PT to ligand.
 XX Example 2; Fig 7; 111pp; English.
 XX
 CC The present invention relates to a method for altering the affinity of a
 CC nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
 CC or in vitro, or reversing the binding of the labelled ligand to a target
 CC tissue. The method comprises administering a modulator that binds to the
 CC ligand to a patient receiving the ligand, or contacting the ligand with
 CC the modulator under conditions such that the modulator binds to the
 CC ligand, and thus alters the affinity of the ligand for the target
 CC molecule. The method is useful for treating a number of disorders e.g.
 CC infection, autoimmunity, tumours, inflammatory proliferative diseases and
 CC hypoglycaemia. The present sequence is an aptamer to human coagulation
 CC factor IXa (FIXa aptamer), which was used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 29 BP; 6 A; 10 C; 8 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 29; DB 7; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.00031;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 GGGGACUAUACCGGCAUUGUGCAUCCCC 29

RESULT 3
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 ID ABZ21258 standard; RNA; 33 BP.
 XX
 AC ABZ21258;
 DT 16-APR-2003 (first entry)
 XX
 DE Aptamer 9.20t, SEQ ID 18.
 XX
 KW Immunosuppressive; aptamer; infection; autoimmunity; tumour;
 KW inflammatory proliferative disease; hypoglycaemia; ss.

Unidentified.
 Key Location/Qualifiers
 FT misc_binding 1..7
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 FT /bound_moiety= "Nucleotides 27..33"
 FT stem_loop 16..25
 FT /tag= b
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WO200296926-A1.
 PN
 XX
 XX 05-DEC-2002.
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 PF 28-MAY-2002; 2002WO-US016555.
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 PR 25-MAY-2001; 2001US-0293231P.
 PR 07-NOV-2001; 2001US-0331037P.
 XX
 PA (UYDU-) UNIV DUKE.

Sullenger BA, Rusconi C;
 PI
 XX
 WPI; 2003-140438/13.

Altering affinity of nucleic acid ligands for target molecules in a
 patient or reversing binding of labeled ligands to target tissues, by
 administering (to a patient receiving the ligand) a modulator that binds
 to ligand.

Example 3; Fig 10A; 11pp; English.

PS The present invention relates to a method for altering the affinity of a
 XX nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
 CC or in vitro, or reversing the binding of the labelled ligand to a target
 CC tissue. The method comprises administering a modulator that binds to the
 CC ligand to a patient receiving the ligand, or contacting the ligand with
 CC the modulator under conditions such that the modulator binds to the
 CC ligand, and thus alters the affinity of the ligand for the target
 CC molecule. The method is useful for treating a number of disorders e.g.
 CC infection, autoimmunity, tumours, inflammatory proliferative diseases and
 CC hypoglycaemia. The present sequence is an aptamer which was used to
 CC illustrate the method of the invention
 XX

Sequence 33 BP; 8 A; 10 C; 8 G; 0 T; 7 U; 0 Other;

Query Match 100.0%; Score 29; DB 7; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGACUUAUACCGGCAUUGUGCAUCCCC 29
 DB 3 GGGGACUUAUACCGGCAUUGUGCAUCCCC 31

RESULT 4

ABN88504
 ID ABN88504 standard; RNA; 96 BP.
 AC ABN88504;

19-AUG-2002 (first entry)

Coagulation_factor Ixa binding/inhibiting RNA aptamer SEQ ID NO:17.

RNA aptamer; identification; coagulation factor; angiopoietin; thrombin;
 E2F family; cardiant; cystostatic; cardiovascular disease; anticoagulant;
 cell proliferation; intimal hyperplasia; angiogenesis;
 bypass graft surgery; ss.

Homo sapiens.

Synthetic.

WO200226932-A2.

04-APR-2002.

26-SEP-2001; 2001WO-US030004.

26-SEP-2000; 2000US-0235654P.

(UYDU-) UNIV DUKE.

Sullenger BA, Rusconi CP;

WPI; 2002-479560/51.

Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
 family members, Ang1 or Ang2, useful for modulating coagulation pathway
 factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.

Claim 13; Fig 1B; 216pp; English.

The present invention describes RNA aptamers (I,II,III) that selectively
 bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
 angiopoietin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
 a dissociation constant for the coagulation pathway factor, an E2F family
 member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
 cardiant and cystostatic activities. (I) are useful for modulating the
 biological activity of a coagulation pathway factor which involves
 administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
 the biological activity of the coagulation pathway factor in the warm-
 blooded vertebrate is modulated. (I) are also useful for treating

CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
 CC activity in a warm-blooded vertebrate. (III) are useful for modulating
 CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
 CC anticoagulants and significantly delay the clotting time of normal human
 CC plasma or the activation of platelets in response to thrombin. (II) are
 CC useful for inhibiting cell proliferation in a number of conditions e.g.,
 CC intimal hyperplasia following bypass graft surgery. (III) are useful for
 CC modulating angiogenesis. The RNA aptamers are also useful as diagnostic,
 CC research and therapeutic context. The aptamers are useful as diagnostic
 CC reagents to detect the presence or absence of target substances to which
 CC they specifically bind, and for identifying substances to which they
 CC specifically bind, for isolating and purifying substances to which they
 CC bind, and as a separation reagent for relieving the targets to which they
 CC they specifically bind. ABN88488 to ABN88713 and ABN81231 represent
 CC sequences used in the exemplification of the present invention
 XX

Sequence 96 BP; 28 A; 25 C; 28 G; 0 T; 15 U; 0 Other;

Query Match 100.0%; Score 29; DB 6; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.00037;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGACUUAUACCGGCAUUGUGCAUCCCC 29

DB 20 GGGGACUUAUACCGGCAUUGUGCAUCCCC 48

RESULT 5

AAT27772/c
 ID AAT27772 standard; cDNA; 169 BP.

AC AAT27772;

15-NOV-1996 (first entry)

Human neural thread protein genomic clone (G5dPet-M13R).

Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
 neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
 binding fragment; ds.

Homo sapiens.

WO9615272-A1.

23-MAY-1996.

14-NOV-1995; 95WO-US017111.

14-NOV-1994; 94US-00340426.

(GEHO) GEN HOSPITAL CORP.

De La Monte S, Wands JR;

WPI; 1996-259865/26.

Detection of neural thread protein in diagnosis of Alzheimer's disease -
 also NTP DNA and protein sequences used in gene and anti-sense therapy.

Disclosure; Fig 22E; 238pp; English.

A method for detecting the presence of neural thread protein (NTP) having
 a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
 comprises (a) contacting a sample from a human subject that is suspected
 of containing the NTP with at least one molecule capable of binding to
 the protein; and (b) detecting any of the molecule bound to the protein.
 The binding molecule is selected from an antibody free of natural
 impurities, a monoclonal antibody or a binding fragment of either of
 these. The method may be used for diagnosing the presence of Alzheimer's
 disease, neuroectodermal tumours and a malignant astrocytoma in a human.
 A number of clones of neural thread protein were isolated from healthy 17
 -18 week old foetal human brain (HB) 2 year old temporal lobe neocortex

CC and end stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75
XX Sequence 169 BP; 48 A; 24 C; 41 G; 56 T; 0 U; 0 Other;
SQ Query Match 65.5%; Score 19; DB 2; Length 169;
Best Local Similarity 70.4%; Pred. No. 29;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 GGACUUAACCGGCAUUGUGCAUCCCC 29
||||| :||| :||| :||| :|||
Db 36 GGACCAAAAGCGGCATCGTGCCTCCC 10

RESULT 6
ID ABN88494 standard; RNA; 96 BP.
XX
AC ABN88494;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:7.
XX
DE RNA aptamer; identification; coagulation factor; angiotensin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX Homo sapiens.
OS Synthetic.
XX
XX WO200226932-A2.
XX
PD 04-APR-2002.
XX
XX 26-SEP-2001; 2001WO-US030004.
XX
XX 26-SEP-2000; 2000US-0235654P.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Sullenger BA, Rusconi CP;
PI
XX WPI; 2002-479560/51.
XX
XX Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Ang1 or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
XX Claim 13; Fig 1A; 216pp; English.

CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiotensin-1 (Ang1) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) are
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating E2F
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they

CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88494 to ABN88713 and ABN81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 96 BP; 24 A; 26 C; 30 G; 0 T; 16 U; 0 Other;
Query Match 61.4%; Score 17.8; DB 6; Length 96;
Best Local Similarity 90.5%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 ACUAUACCGGCAUUGUGCAU 25
||||| :||| :||| :||| :|||
Db 30 ACUAUACCGGCAUUGUGCAU 50

RESULT 7
ID AAX11804 standard; DNA; 101 BP.
XX
AC AAX11804;
XX
XX 30-MAR-1999 (first entry)
XX
XX Human biallelic polymorphic DNA fragment WI-18680.
XX
DE Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW detection; phenotypic typing; characteristic; infection; hereditary;
KW autoimmune disease; cancer; inflammation; drug; therapy; medication;
KW treatment; marker; ss.
XX Homo sapiens.
OS
XX WO9820165-A2.
XX
XX 14-MAY-1998.
XX
XX 05-NOV-1997; 97WO-US020313.
XX
XX 06-NOV-1996; 96US-0030455P.
XX
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Lander ES, Wang D, Hudson T;
PI
XX WPI; 1998-286974/25.
XX
XX New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
XX
XX Claim 1; Page 195; 310pp; English.

XX AAX10269-X12937 are human DNA fragments which contain biallelic
XX polymorphic markers which have been isolated using the primers
CC represented in AAX09121-X10268. The base occupying the polymorphic site
CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC can be used in methods for determining polymorphic forms in an individual
CC for use in e.g. forensics, paternity testing or for phenotypic typing for
CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC familial hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
SQ Sequence 101 BP; 27 A; 23 C; 26 G; 24 T; 0 U; 1 Other;

Query Match 61.4%; Score 17.8; DB 2; Length 101;
Best Local Similarity 62.1%; Pred. No. 1e+02;
Matches 18; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGACUUAUACCGGCAUUGGCAUCC 29
DB 11 GAGTACTGTACACGCAAGCATGCATCCCC 39

RESULT 8

AD35061
ID ADE35061 standard; DNA; 166 BP.

XX AC ADE35061;

XX 29-JAN-2004 (first entry)

XX Mouse fibroblast growth factor-4 promoter.

XX Fibroblast growth factor-4; FGF-4; mouse; stem cell; promoter; ds.

XX Mus sp.

XX WO2003080816-A2.

XX 02-OCT-2003.

XX 18-MAR-2003; 2003WO-GB001111.

XX 19-MAR-2002; 2002GB-00006422.

XX 08-MAY-2002; 2002GB-00010458.

XX (UYSH-) UNIV SHEPFIELD.

XX Andrews P, Draper J;

XX WPI; 2003-779256/73.

XX Manipulating phenotype of stem cell by providing cell transfected with

XX nucleic acid comprising promoter which confers substantial stem cell

XX specific expression on selective marker gene(s), and proliferating cell.

XX Disclosure; Fig 2; 40pp; English.

XX The present sequence is that of the mouse fibroblast growth factor-3 (FGF

XX -4) promoter from nucleotides -64 to +101. Transcription factor binding

XX motifs ADE35058-ADE35060 from FGF-4 promoters have been shown to direct

XX stem cell specific expression. This discovery has been shown in methods of

XX the invention for manipulating the phenotype of a stem cell. In such a

XX method, a cell is transfected with a nucleic acid molecule that includes

XX a promoter which comprises a motif that confers stem cell specific

XX expression on a selectable marker (e.g. fluorescent protein or produg

XX activating polypeptide) gene, and conditions conducive to proliferation

XX of the cell are provided. A cell culture system is provided which

XX facilitates the maintenance of stem cells, particularly embryonic stem

XX cells, in an undifferentiated state. Also provided are differentiated

XX cells and tissues, the genome of which includes a nucleic acid construct

XX comprising a promoter which has a stem cell specific expression pattern

XX which controls expression of a gene the expression of which allows the

XX selective ablation of cells which have de-differentiated to a stem cell

XX phenotype, thereby allowing their removal from a population of

XX differentiated cells. The stem cells are haematopoietic, neural, bone,

XX muscle, mesenchymal, trophoblastic, epithelial, endodermal or embryonic

XX stem cells (including embryonal carcinoma TERA2 or NTERA2 cells), or

XX embryonal germ cells.

XX Sequence 166 BP; 27 A; 57 C; 53 G; 29 T; 0 U; 0 Other;

Query Match 57.9%; Score 16.8; DB 9; Length 166;

Best Local Similarity 60.7%; Pred. No. 3.4e+02;

Matches 17; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGACUUAUACCGGCAUUGGCAUCC 28
DB 67 GGGGACTATCCCGCCACCGTTGCGTCCC 94

RESULT 9

AD35062

ID ADE35062 standard; DNA; 181 BP.

XX AC ADE35062;

XX 29-JAN-2004 (first entry)

XX Mouse fibroblast growth factor-4 promoter.

XX Fibroblast growth factor-4; FGF-4; mouse; stem cell; promoter; ds.

XX Mus sp.

XX WO2003080816-A2.

XX 02-OCT-2003.

XX 18-MAR-2003; 2003WO-GB001111.

XX 19-MAR-2002; 2002GB-00006422.

XX 08-MAY-2002; 2002GB-00010458.

XX (UYSH-) UNIV SHEPFIELD.

XX Andrews P, Draper J;

XX WPI; 2003-779256/73.

XX Manipulating phenotype of stem cell by providing cell transfected with

XX nucleic acid comprising promoter which confers substantial stem cell

XX specific expression on selective marker gene(s), and proliferating cell.

XX Disclosure; Fig 2; 40pp; English.

XX The present sequence is that of the mouse fibroblast growth factor-3 (FGF

XX -4) promoter from nucleotides -64 to +116. Transcription factor binding

XX motifs ADE35058-ADE35060 from FGF-4 promoters have been shown to direct

XX stem cell specific expression. This discovery has been shown in methods of

XX the invention for manipulating the phenotype of a stem cell. In such a

XX method, a cell is transfected with a nucleic acid molecule that includes

XX a promoter which comprises a motif that confers stem cell specific

XX expression on a selectable marker (e.g. fluorescent protein or produg

XX activating polypeptide) gene, and conditions conducive to proliferation

XX of the cell are provided. A cell culture system is provided which

XX facilitates the maintenance of stem cells, particularly embryonic stem

XX cells, in an undifferentiated state. Also provided are differentiated

XX cells and tissues, the genome of which includes a nucleic acid construct

XX comprising a promoter which has a stem cell specific expression pattern

XX which controls expression of a gene the expression of which allows the

XX selective ablation of cells which have de-differentiated to a stem cell

XX phenotype, thereby allowing their removal from a population of

XX differentiated cells. The stem cells are haematopoietic, neural, bone,

XX muscle, mesenchymal, trophoblastic, epithelial, endodermal or embryonic

XX stem cells (including embryonal carcinoma TERA2 or NTERA2 cells), or

XX embryonal germ cells.

XX Sequence 181 BP; 27 A; 63 C; 62 G; 29 T; 0 U; 0 Other;

Query Match 57.9%; Score 16.8; DB 9; Length 181;

Best Local Similarity 60.7%; Pred. No. 3.4e+02;

Matches 17; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGGGACUUAUACCGGCAUUGGCAUCC 28
DB 67 GGGGACTATCCCGCCACCGTTGCGTCCC 94

```
RESULT 10
ABZ21255
ID ABZ21255 standard; RNA; 29 BP.
XX
AC ABZ21255;
XX
DT 16-APR-2003 (first entry)
XX
DE FIXa aptamer, SEQ ID 15.
XX
KW Immunosuppressive; aptamer; infection; autoimmunity; tumour;
KW inflammatory proliferative disease; hypoglycaemia; human;
KW coagulation Factor IXa; FIXa; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_binding 1..5
FT /tag= a
FT /bound_moiety= "Nucleotides 25..29"
FT stem_loop 11..21
FT /tag= b
FT misc_binding 25..29
FT /tag= c
FT /bound_moiety= "Nucleotides 1..5"
XX
PN WO200296926-A1.
XX
PD 05-DEC-2002.
XX
PF 28-MAY-2002; 2002WO-US016555.
XX
PR 25-MAY-2001; 2001US-0293231P.
PR 07-NOV-2001; 2001US-0331037P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi C;
XX
WPI; 2003-140438/13.
XX
PT Altering affinity of nucleic acid ligands for target molecules in a
PT patient or reversing binding of labeled ligands to target tissues, by
PT administering (to a patient receiving the ligand) a modulator that binds
PT to ligand.
XX
PS Example 2; Fig 7; ilpp; English.
XX
CC The present invention relates to a method for altering the affinity of a
CC nucleic acid ligand (e.g. an aptamer) for a target molecule in a patient
CC or in vitro, or reversing the binding of the labelled ligand to a target
CC tissue. The method comprises administering a modulator that binds to the
CC ligand to a patient receiving the ligand, or contacting the ligand with
CC the modulator under conditions such that the modulator binds to the
CC ligand, and thus alters the affinity of the ligand for the target
CC molecule. The method is useful for treating a number of disorders e.g.
CC infection, autoimmunity, tumours, inflammatory proliferative diseases and
CC hypoglycaemia. The present sequence is an aptamer to human coagulation
CC Factor IXa (FIXa aptamer), which was used to illustrate the method of the
CC invention
XX
SQ Sequence 29 BP; 8 A; 8 C; 8 G; 0 T; 5 U; 0 Other;
Query Match 55.9%; Score 16.2; DB 7; Length 29;
Best Local Similarity 72.4%; Pred. No. 5.1e+02;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 GGGGACUAUACCGGAUUCGUGCAUCCCC 29
| | | | | | | | | | | | | | | | | | | |
Db 1 GGGGACUAUACCGGAUUCGUGCAUCCCC 29
| | | | | | | | | | | | | | | | | | | |
RESULT 11
ABN88499
ID ABN88499 standard; RNA; 95 BP.
XX
AC ABN88499;
XX
DT 19-AUG-2002 (first entry)
XX
DE Coagulation factor IXa binding/inhibiting RNA aptamer SEQ ID NO:12.
XX
KW RNA aptamer; identification; coagulation factor; angiotensin; thrombin;
KW E2F family; cardiant; cytostatic; cardiovascular disease; anticoagulant;
KW cell proliferation; intimal hyperplasia; angiogenesis;
KW bypass graft surgery; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200226932-A2.
XX
PD 04-APR-2002.
XX
PF 26-SEP-2001; 2001WO-US030004.
XX
PR 26-SEP-2000; 2000US-0235654P.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Sullenger BA, Rusconi CP;
XX
WPI; 2002-479560/51.
XX
PT Novel RNA aptamers that selectively bind coagulation pathway factors, E2F
PT family members, Angi or Ang2, useful for modulating coagulation pathway
PT factor activity, E2F activity and Ang1 or Ang2 activity in a mammal.
XX
PS Claim 13; Fig 1A; 216pp; English.
XX
CC The present invention describes RNA aptamers (I,II,III) that selectively
CC bind: (a) a coagulation pathway factor; (b) an E2F family member; or (c)
CC angiotensin-1 (Angi) or Ang2, respectively, where (I), (II), (III) have
CC a dissociation constant for the coagulation pathway factor, an E2F family
CC member, or Ang1 or Ang2 of about 20 nM or less. (I), (II) and (III) have
CC cardiant and cytostatic activities. (I) are useful for modulating the
CC biological activity of a coagulation pathway factor which involves
CC administering (I) to a warm-blooded vertebrate (e.g., a mammal) such that
CC the biological activity of the coagulation pathway factor in the warm-
CC blooded vertebrate is modulated. (I) are also useful for treating
CC cardiovascular diseases in the mammal. (II) are useful for modulating
CC activity in a warm-blooded vertebrate. (III) are useful for modulating
CC Ang1 or Ang2 activity in a warm-blooded vertebrate. (I) are potent
CC anticoagulants and significantly delay the clotting time of normal human
CC plasma or the activation of platelets in response to thrombin. (II) are
CC useful for inhibiting cell proliferation in a number of conditions e.g.,
CC intimal hyperplasia following bypass graft surgery. (III) are useful for
CC modulating angiogenesis. The RNA aptamers are also useful for diagnostic,
CC research and therapeutic context. The aptamers are useful as diagnostic
CC reagents to detect the presence or absence of target substances to which
CC they specifically bind, and for identifying substances to which they
CC specifically bind, for isolating and purifying substances to which they
CC bind, and as a separation reagent for retrieving the targets to which
CC they specifically bind. ABN88488 to ABN88713 and ABN81231 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 95 BP; 25 A; 26 C; 29 G; 0 T; 15 U; 0 Other;
Query Match 55.9%; Score 16.2; DB 6; Length 95;
Best Local Similarity 72.4%; Pred. No. 6.1e+02;
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 GGGGACUAUACCGGAUUCGUGCAUCCCC 29
| | | | | | | | | | | | | | | | | | | |
Db 20 GGGGACUAUACCGGAUUCGUGCAUCCCC 48
| | | | | | | | | | | | | | | | | | | |
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RESULT 12
 ABX91389
 ID ABX91389 standard; cDNA; 172 BP.
 XX AC ABX91389;
 XX DT 07-MAY-2003 (first entry)
 XX DE Murine gene trapped sequence (GTS) SEQ ID NO 733.
 XX KW Murine; mouse; gene trap technology; gene trapped sequence; GTS;
 KW gene identification; functional genomic analysis; gene discovery;
 KW gene expression analysis; cross species hybridisation analysis;
 KW antisense inhibition; gene targeting; gene; ss.
 XX OS Mus sp.
 XX PN US2002161207-A1.
 XX PD 31-OCT-2002.
 XX PF 30-NOV-2000; 2000US-00728444.
 XX PR 01-DEC-1999; 99US-0168360P.
 XX PA (FRIE/) FRIEDRICH G.
 PA (ZAMB/) ZAMBROWICZ B.
 PA (SAND/) SANDS A T.
 XX PI Friedrich G, Zambrowicz B, Sands AT;
 XX WPI; 2003-288124/28.
 XX PT New murine polynucleotides comprising gene trapped sequences, useful in
 PT functional genomic analysis, in the development of new therapeutic or
 PT diagnostic agents, for diagnostic gene expression analysis or for genetic
 PT manipulations.
 XX PS Claim 2; SEQ ID NO 733; 29pp; English.
 XX CC The present invention relates to novel murine cDNAs produced using gene
 CC trap technology. The OMNIBANK gene trapped sequences (GTSs) are
 CC individually identified novel genes, and are useful in functional genomic
 CC analysis, in the discovery and development of new therapeutic and
 CC diagnostic agents, for gene discovery, for diagnostic gene expression
 CC analysis, for cross species hybridisation analysis, and for genetic
 CC manipulations such as antisense inhibition or gene targeting. The
 CC polynucleotides of the invention are also useful for isolating cDNAs,
 CC genomic clones or full-length genes/polynucleotides, or their homologues,
 CC heterologues, paralogues or orthologues, that are capable of hybridising
 CC to one or more of the new murine polynucleotide sequences. The
 CC polynucleotides are also useful for identifying the coding regions of the
 CC murine genome, and as hybridisation probes. ABX90657-ABX91862 represent
 CC the murine GTSs of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipdsIDEntry.html
 XX SQ Sequence 172 BP; 51 A; 53 C; 38 G; 26 T; 0 U; 4 Other;
 Query Match 55.2%; Score 16; DB 7; Length 172;
 Best Local Similarity 60.0%; Pred. No. 8.3e+02;
 Matches 15; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 3 GGACUUAACGGCAUUGGCAUCC 27
 DB 90 GGANGATACCTTCAGTCCTGCATCC 114
 RESULT 13
 ABZ01528/c
 ID ABZ01528 standard; DNA; 50 BP.

XX ABZ01528;
 XX AC 09-JAN-2003 (first entry)
 XX DT Human leukocyte gene expression profiling probe SEQ ID NO 1519.
 XX DE T7; leukocyte; gene expression profiling; allograft rejection;
 KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
 KW ss.
 XX OS Homo sapiens.
 XX PN WO200257414-A2.
 XX PD 25-JUL-2002.
 XX PF 22-OCT-2001; 2001WO-US047856.
 XX PR 20-OCT-2000; 2000US-0241994P.
 XX PR 08-JUN-2001; 2001US-0296764P.
 XX PA (BIOC-) BIOCARDIA INC.
 XX PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
 PI Ly N, Woodward R, Quettermous T, Johnson F;
 XX WPI; 2002-636525/58.
 XX PT New system for leukocyte expression profiling, diagnosing a disease, or
 PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis
 PT or congestive heart failure, comprises diagnostic oligonucleotides.
 XX PS Claim 1; Page 374; Opp; English.
 XX CC The invention relates to a system for detecting gene expression, which
 CC comprises one or two isolated DNA molecules that detect expression of a
 CC gene, where the gene corresponds to any of 8143 oligonucleotides
 CC (ABZ00010-ABZ008152) each having 50 base pairs (bp). The system is useful
 CC for leukocyte expression profiling. It is particularly useful for
 CC diagnosing a disease, monitoring (rate of) progression of a disease,
 CC predicting therapeutic outcome, determining prognosis for a patient,
 CC predicting disease complications in an individual or monitoring response
 CC to treatment in an individual. The diseases include cardiac allograft
 CC rejection, kidney allograft rejection, liver allograft rejection,
 CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
 XX SQ Sequence 50 BP; 8 A; 8 C; 15 G; 19 T; 0 U; 0 Other;
 Query Match 54.5%; Score 15; DB 6; Length 50;
 Best Local Similarity 63.0%; Pred. No. 8.7e+02;
 Matches 17; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 3 GGACUUAACGGCAUUGGCAUCC 29
 DB 37 GGACCATATCAGCAATGAGGCATCACC 11
 RESULT 14
 ADA01911/c
 ID ADA01911 standard; DNA; 105 BP.
 XX AC ADA01911;
 XX DT 06-NOV-2003 (first entry)
 XX DE Mouse carcinoma associated nucleic acid, SEQ ID NO:430.
 XX KW Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
 KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
 KW ds.

XX	Mus sp.
XX	WO2003057146-A2.
XX	PN
XX	PD
XX	17-JUL-2003.
XX	26-DEC-2002; 2002WO-US041414.
XX	PF
XX	PR
XX	26-DEC-2001; 2001US-00035832.
XX	(SAGR-) SAGRES DISCOVERY.
XX	PA
XX	Pi
XX	PI
XX	Morris DW;
XX	WPI; 2003-587068/55.
XX	DR
XX	PT
XX	New recombinant nucleic acid encoding carcinoma associated protein,
XX	useful for preparing compositions for treating carcinomas.
XX	PS
XX	Claim 1; Page 185; 245pp; English.
XX	CC
XX	The invention relates to recombinant carcinoma associated (CA) nucleic
XX	acid sequences from mouse and human (ADA01482-ADA03094), and to
XX	recombinant carcinoma associated proteins (CAP) encoded by them. The
XX	invention also encompasses expression vectors and host cells comprising a
XX	CA nucleic acid, a polypeptide (especially an antibody) that specifically
XX	binds to the protein, and a biochip comprising CA nucleic acid or
XX	fragments thereof. The sequences of the invention were identified using
XX	oncogenic retroviruses, which insert into the genome of the host organism
XX	at random. Many of these do not carry transduced host oncogenes or
XX	pathogenic trans-acting viral genes, meaning that cancer incidence is a
XX	direct consequence of the effects of proviral integration into host
XX	protooncogenes. The CA nucleic acid sequences can be used to diagnose
XX	carcinoma (especially breast cancer, prostate cancer, lymphoma or
XX	leukaemia) or a propensity to carcinoma by determination of the sequence
XX	of a CA gene, or by determination of CA gene expression in particular
XX	tissues. CA nucleic acids, proteins and antibodies are also useful as
XX	therapeutic agents and in screening and evaluating drug candidates. The
XX	present sequence represents a specifically claimed murine CA nucleic acid
XX	sequence of the invention. Note: The sequence data for this patent is
XX	also available in electronic format from WIPO at
XX	ftp.wipo.int/pub/published_pct_sequences.
XX	SQ
XX	Sequence 105 BP; 34 A; 21 C; 29 G; 21 T; 0 U; 0 Other;
Query Match	54.5%; Score 15.8; DB 8; Length 105;
Best Local Similarity	73.7%; Pred. No. 9.7e+02;
Matches 14; Conservative	3; Mismatches 2; Indels 0; Gaps 0;
QY	2 GGGACUUAUCGCGCAAUCG 20
Dd	: : : : : :
	27 GGTTACTATCTGGCAATCG 9
RESULT 15	
ADB71650/c	ID
ID	ADB71650 standard; DNA; 105 BP.
XX	AC
AC	ADB71650;
XX	DT
DT	04-DEC-2003 (first entry)
XX	DE
DE	Mouse carcinoma associated gene fragment #430.
XX	KW
KW	mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
KW	cancer; neoplasm; adenocarcinoma; sarcoma.
OS	Mus sp.
OS	WO2003008583-A2.
PN	30-JAN-2003.
XX	PD